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SEP 1 7 2001





NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

| 水 | 1. | This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's |
|-----|----------|--|
| (—) | | attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990. |
| B | 2. | This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c). |
| R | 3. | A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e). |
| | 4. | A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." |
| | 5. | The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d). |
| | 6. | The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e). |
| | 7. | Other: |
| A m | _1: | cent Must Provide |
| Ap | | cant Must Provide: |
| A | Αı | n <u>initial</u> or substitute computer readable form (CRF) copy of the "Sequence Listing". |
| 8 | Ar in | n <u>initial</u> or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry to the specification. |
| Ø | ap | statement that the content of the paper and computer readable copies are the same and, where oplicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 325(b) or 1.825(d). |
| For | q | uestions regarding compliance to these requirements, please contact: |
| For | R | ules Interpretation, call (703) 308-4216 |
| | | RF Submission Help, call (703) 308-4212 |
| | | atentln software help, call (703) 308-6856 |

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Table VII A Mage 2 A01 Supermotif Peptides with Binding Data

Sequence

SEQ ID NO.

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| 01 to 4 to 1 | 0 / 8 0 0 2 2 2 2 4 5 | 5 | 2 4 2 2 2 4 3 3 6 4 3 3 6 6 6 6 6 6 6 6 6 6 6 6 6 | 32 33 33 34 34 37 |
|--|--|---|--|--|
| 0.1700 | 0.0028 | 0.0450 | 0.0430 | 0,2000 |
| 6 0 0 ∞ 0 0 | 2==020=02= | :2∞ <u>-</u> 20 o o | 00000000 | ∘ o ∞ o ∞ ∑ ∞ ∑ |
| 154 68 249 224 115 | 229 168 168 263 263 63 177 177 | 292 245 246 246 116 178 | 148 260 96 69 72 138 138 | 149 139 139 179 166 166 |
| ASEYLQLVF ASSFSTINY DLVQENYLEY ELSMLEVF ELSMLEVF ELSMLEVF | ESVLRNCQDF EVFEGREDSVF EVPUSHLY FSTTINYTLW GSDPACYEF GSDPACYEFLW ILVTCLGLSY ILVTCLGLSY ISRKMVFLVHF | KIGGEPHISY KMVELVHF LLMQDLVQENY LVHFLLLKY LVQENYLEXY LVQENYLEXY LVQENYLEY | PVIFSKASEY QVPGSDPACY QVPGSDPACY SSESTIINY STTINYTLW SYLRNÇQDF SVLRNÇQDF | VIESKASEY VLRNCQDF VLRNCQDFF VTCLGLSY VVEVVPISHLY VVPISHLY YILVTCLGLSY |

| Sequence Position No of Amino Actids A-10101 SEQ 1D NO. ASSLCHTMANY 68 10 2.6000 38 ASSLCLALSY 154 9 0.1100 34 ATCLIGLSY 113 10 4.0 4.0 ATCLIGLSY 113 10 0.1100 4.0 ATCLIGLSY 113 10 0.1100 4.0 ATCLIGLSY 114 10 0.1100 4.0 ATCLIGLSY 114 10 0.100 4.0 ATCLIGLSY 114 10 0.100 4.0 ATCLIGLSY 114 10 0.000 4.0 ATCLIGLSY 114 10 0.000 4.0 ATCLIGLSY 117 11 0.000 4.0 4.0 ATCLIGLSY 117 11 0.000 0.000 4.0 4.0 ATCLIGLSY 117 11 0.000 0.000 4.0 4.0 4.0 4.0 4.0 4.0 </th <th></th> <th></th> <th></th> <th>٠</th> <th></th> | | | | ٠ | |
|--|---------------|--------------|-----------------------|---------|------------|
| 68 10 2 6000 154 9 0 11100 155 179 8 8 011100 151 115 100 152 153 9 9 111 152 153 9 9 100 153 154 111 155 155 9 9 100 155 155 9 9 100 155 155 9 9 100 155 155 155 9 9 100 155 155 155 9 9 100 155 155 155 155 155 155 155 155 155 155 | nce | Position | No. of Amino Acids | A*0101 | SEQ ID NO. |
| 154 9 0.1100 124 15 16 18 19 158 19 10 18 158 19 10 18 158 19 10 18 159 19 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 10 150 150 10 150 10 10 | PTTMNY | 89 | 01 | 2.6000 | 38 |
| 224 8 8 01100 1154 18 8 01100 1168 19 10 18 18 30000 168 19 10 18 18 30000 225 25 3 11 1 10 10 10 10 10 10 10 10 10 10 10 1 | -QLVF | 154 | 6 | | 33 |
| 1154 10 8 8 18 18 18 18 18 18 18 18 18 18 18 18 | GLSY | 179 | œ | 0.1100 | 40 |
| 115 10 11 11 11 11 11 11 11 11 11 11 11 11 | LEVF | 224 | ∞ | | 41 |
| 154 10 10 18,0000 16,000 16,000 16,000 16,000 16,000 16,000 17,00 | FLLLKY | 115 | 10 | | 42 |
| 168 9 18,000 18,000 18,000 19,000 | SVVCNW | 134 | 2 | | £3 |
| 168 111 263 9 9 264 11 000500 137 137 10 9 298 10 00011 298 10 00011 299 10 00011 246 111 00001 246 111 00001 250 9 9 00011 247 111 8 8 250 9 9 00001 250 9 9 00001 260 8 8 8 8 260 8 8 8 8 27 | IGHLY | 168 | 6 | 18.0000 | 44 |
| 250 263 11 137 11 137 11 137 11 12 298 10 11 299 10 00370 2039 203 2045 11 245 11 246 11 11 250 260 11 11 260 11 11 260 11 11 260 11 11 260 11 11 260 11 11 260 11 11 260 11 11 260 11 11 260 11 11 260 260 260 260 260 260 260 260 260 260 | IGHLYIF | 891 | = | | 45 |
| 255 265 1137 1137 115 27 286 287 287 287 287 287 287 287 287 287 287 | NYLEY | 250 | σ. | | 46 |
| 7 137 9 11 100000000000000000000000000000000 | ACYEF | 763 | ς: | | 47 |
| 137 19 0 00500 137 110 11 139 293 9 9 0 00370 209 209 9 0 00370 209 209 10 0 11 212 245 11 11 11 246 11 11 11 246 11 11 11 246 11 11 11 246 11 11 11 247 11 8 8 250 260 10 11 250 260 260 260 29 9 260 20 20 260 20 20 260 20 20 270 28 20 280 20 290 20 200 20 200 20 200 20 200 20 200 20 200 20 200 20 200 20 200 20 200 20 200 200 200 2 | ACYEFLW | 263 | | | 48 |
| 137 110 298 100 299 9 9 00370 299 9 9 00011 245 111 | GNWQY | 137 | ø | 0.0500 | 49 |
| Y 137 111 Y 138 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | GNWQYF | 137 | 01 | | 20 |
| 298 10 00370 299 9 0 00011 112 8 8 00011 114 11 7.5000 116 109 111 7.5000 117 8 9 0.2600 118 9 9 0.2500 119 111 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | 'GNWQYFF | 137 | = | | 15 |
| 293 9 9 00370 294 10 10 00011 112 8 8 75000 116 9 9 0.2600 117 8 8 8 8 10 0.0550 118 8 8 8 138 8 8 10 0.0550 119 8 8 138 8 8 10 0.0550 138 8 8 138 139 9 9 0.0550 | PLHEW | 298 | 01 | | 52 |
| 299 9 0 0.0011 112 8 8 0.0011 113 8 134 Y 135 9 9 0.2600 Y 135 9 9 0.2600 Y 131 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | PHISY | 293 | 6 | 0.0370 | 53 |
| 792 10 0.0011 245 11 8 7.500 109 11 7.500 246 11 0 0.2600 247 135 11 0.2600 70 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | LHEW | 299 | 6 | | 54 |
| 112 8 8 1.5000 1.5000 1.10 1.10 1.5000 1.10 1.1 | SPHISY | 292 | 10 | 0.0011 | 55 |
| 11 7.5000 109 111 0.2600 246 10 10 0.2600 116 9 9 117 8 8 17 8 8 18 8 10 0.0550 10 0.0550 11 0.0830 11 0.0830 | CLVHF | 112 | : ∞ | | 56 |
| 166 11 | HFVQENY | 245 | == | | 57 |
| 109 | /DPIGHLY | 991 | = | 7,5000 | 58 |
| 146 10 0.2600 116 9 0.2600 135 9 11 171 8 11 250 10 11 70 11 0.0550 155 8 8 96 9 0.0550 138 8 10 138 9 11 139 8 10 139 8 8 139 8 8 139 8 8 139 8 8 | VAELVHF | 109 | = | | 59 |
| 116 9 9 9 9 9 9 9 9 9 | FVQENY | 246 | 10 | 0.2600 | 09 |
| Y 135 9 135 11 18 8 72 9 72 9 70 8 69 9 155 8 160 18 9 138 8 138 9 139 8 139 8 139 8 | LLLKY | 911 | 6 | | 19 |
| Y 135 11 8 8 8 8 10 0.0550 138 8 8 8 138 9 9 139 139 8 8 8 139 9 139 9 139 9 139 9 139 9 139 9 139 9 9 | SVVGNW | 135 | 6 | | 62 |
| 171 8 95 11 72 9 260 10 70 11 69 9 96 10 138 8 138 9 138 10 7 7 4 11 139 8 139 9 | WONWOY | 135 | = | | 63 |
| 95 11 72 9 260 10 70 8 70 8 8 8 155 8 8 8 10 0.0550 74 11 0.0830 73 8 8 8 138 9 140 0.0830 | CYIF | 171 | 8 | | 49 |
| 72 9 9 70 10 10 10 10 10 10 10 10 10 10 10 10 10 | PDLESEF | 95 | = | | 65 |
| 260 10 8 8 0.0550 155 | INYPLW | 72 | 6 | | : % |
| 70 8 8 0.0550 69 9 0.0550 155 8 8 8 138 8 8 138 9 0.0830 7 7 4 11 0.0830 | SDPACY | 260 | 10 | | 29 |
| 70 11 0.0550 69 9 0.0550 155 8 8 138 8 8 138 9 9 138 10 7 74 11 0.0830 | TMNY | 70 | . ∞ | | . % |
| 69 9 0.0550 155 8 0.0550 96 10 138 8 8 138 9 9 17 74 11 0.0830 139 8 8 | TMNYPLW | 70 | . = | | 69 |
| F 138 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | TIMNY | : 69 | : 0 | 0.0550 | 92 |
| 96 10 138 8 138 8 138 10 5Y 74 11 0.0830 139 8 | 3 VF | \$ <u>\$</u> | · œ | 00000 | 2.2 |
| 138 8 138 8 138 9 5Y 74 11 0.0830 5Y 73 8 139 8 | DIESEF | £ 56 | » <u>c</u> | | |
| F 138 9 9 0.0830 SY 74 11 0.0830 8 8 139 8 139 9 9 | NWO | 138 | ? ∝ | | 1 (|
| F 138 10 SY 74 11 0.0830 73 8 8 139 8 9 | NWOYF | 38 | o | | 27 |
| Y 74 (1 0.0830 73 8 8 139 8 | NWOYFF | 3 6 6 | . 2 | | 75 |
| 73 8 139 8 F 139 9 | PLWSOSY | 74 | Ξ | 0.0830 | 92 |
| 139 8 F 139 9 | IYPLW | 73 | 8 | | 77 |
| 139 9 | IWQYF | 139 | ∞ | | 78 |
| | VVGNWQYFF | 139 | 6 | | 79 |

| | f with Binding Data |
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| | 1 |
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| Table VIII | _ |
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| | 4 |
| | 9 |
| | Mage 2 A02 Supermotif |
| | |
| | |

| | SEQ ID NO. | 25 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 |
|---|-----------------------|---|
| | A*6802 | |
| | A*0206 | |
| ith Binding Data | A*0203 | |
| Mage 2 A02 Supermotif with Binding Data | A*0202 | |
| Mage 2 A | A*0201 | |
| | No. of Amino Acids | ∞2 <u></u> |
| | Position | 107 107 108 108 107 107 108 108 108 108 108 108 108 108 108 108 |
| | Sequence | AAISKKMV AAISKKMVEL AAISKKMVEL AIIAIEGDCA AIIAIEGDCA AIIAIEGDCA ALIGLVGAQA ALIGTSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW ALIETSYW CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGLSYDGL CCGSEFQA DLESEFQA DLESEFQA DLESEFQA DLESEFQA DLESEFQA DLESEFQA DLESEFQA DLESEFQA DLESEFQA EAGGALGL EVVEVVPISHL EVVEVVPISHL EVVEVVPISHL EVVEVNPISHL EVVEVNPISHL EVVEVNPISHL EVVENPISHL E |

Table VIII A
Mage 2 A02 Supermotif with Binding Data

| | | | Mage 2 A(| Mage 2 A02 Supermotif with Binding Data | th Binding Data | | | |
|-----------------------|------------|-----------------------|-----------|---|-----------------|--------|--------|------------|
| Sequence | Position | No. of Amino Acids | A*0201 | A*0202 | A*0203 | A*0206 | A*6802 | SEQ ID NO. |
| GASSFSTT | 67 | 8 | | | | | | 127 |
| GASSFSTTI | 29 | 6 | | | | | | 128 |
| GIEVVEVV | <u> </u> | ∞ ; | | | | | | 129 |
| GIEVVEVVPI | 50. | 2 6 | | | | | | 130 |
| GLEANGEA GLEARGEAI | C 2 | ∞ c | | | | | | 131 |
| GLEARGEALGI | <u> </u> | ^ = | | | | | | 132 |
| GLEGONOV | 287 | <u> </u> | | | | | | 133 |
| GLEGDNOVM | 88 | oo | | | | | | 134 |
| GLLIIVLA | 200 | · oc | | | | | | 251 |
| GLLIIVLAI | 200 | 0 | | | | | | 132 |
| GLLIIVLAII | 200 | 01 | | | | | | 138 |
| GLLIIVLAIIA | 200 | = | | | | | | 139 |
| GLSYDGLL | 183 | ∞ | | | | | | 140 |
| GLVGAQAPA | 77 | 6 | | | | | | 141 |
| GLVGAQAPAT | 24 | 0. | | | | | | 142 |
| HISYPPLHEKA | 298 | = • | | | | | | 143 |
| HLYILVICL | 4/1 | ъ.; | | | | | | 144 |
| HETELY ICEGE | 4/- | = = | | | | | | 145 |
| HICKIGGERAL | 687 | = • | | | | | | 146 |
| HATEGOOA | 208 | • • | | | | | | 147 |
| IIVIAIIA | 203 | · ∝ | | | | | | 84. |
| IIVLAIIAI | 203 | . 6 | | | | | | 149 |
| ILVTCLGL | 171 | - 00 | | | | | | 3 5 |
| IVLAIIAI | 204 | 8 | | | | | | 152 |
| KAEMLESV | 132 | ∞ | | | | | | 153 |
| KAEMLESVL | 132 | 6 | | | | | | 154 |
| KASEYLQL | 55 | ∞ ∘ | | | | | | 155 |
| KASEYLŲLV | 153 | σ. | | | | | | 156 |
| KIGGEFFI | 292 | × • | | | | | | 157 |
| NIWEELSIM | 077 | × 0 < | | | | | | 158 |
| NIWEELSML | 077 | ν; | | | | | | 159 |
| NIWEELSIMLEV | 077 | _ • | | | | | | 091 |
| KAVELVIER | ‡ <u>:</u> | 60 | | | | | | 191 |
| KMVELVIIFE | 711 | ~ | | | | | | 162 |
| KMVELVIIFEL | 711 | 2: | | | | | | 163 |
| KTGI I IIV | 761 | <u> </u> | | | | | | <u>4</u> |
| KTGLIIVI | 801 | . 0 | | | | | | <u>6</u> |
| KTGI I IIVI A | 861 | · 5 | | | | | | 99 |
| KTGLLIIVLAI | 86 | 2 = | | | | | | /91 |
| KVLHHTLKI | 285 | : 6 | | | | | | 90.7 |
| LAIIAIEGDCA | 206 | = | | | | | | 170 |
| LIETSYVKV | 278 | 6 | | | | | | 171 |
| LIETSYVKVL | 278 | 0 | | | | | | 172 |

Table VIII A
Mage 2 A02 Supermotif with Binding Data

| | SEQ ID NO. | 174 174 174 175 177 177 178 178 178 178 178 178 178 178 |
|---|-----------------------|---|
| | A*6802 | |
| E. | A*0206 | |
| Mage 2 A02 Supermotif with Binding Data | A*0203 | |
| e 2 A02 Supermoti | A*0202 | |
| Mag | A*0201 | - - |
| | No. of Amino Acids | & \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ |
| | Position | 202 202 202 202 202 203 203 203 204 205 205 207 207 207 208 208 208 208 208 208 208 208 208 208 |
| • | Sequence | LIIVLAIII LIIVLAIIA LIIDUQVM LLGDNQVM LLGDNQVM LLGDNQVMPKT LLIIVLAIIA LLIIVLAIIA LLIIVLAIIA LLIIVLAIIA LLIIVLAIIA LLIIVLAIIA LLIIVLAIIA LLIIVLAIIA LLIKYRAREPV LLKYRAREPV LVGUSVV LVGQAPT LVGUSV |

Table VIII A
Mage 2 A02 Supermotif with Binding Data

| SEQ ID NO. | 210 2210 2222 2332 2332 2332 2333 2333 2 |
|-----------------------|--|
| A*6802 | |
| A*0206 | |
| A*0203 | |
| A*0202 | |
| A*0201 | |
| No. of Amino Acids | |
| Position | 29 159 159 159 159 159 159 159 159 159 15 |
| Sequence | QAPATEEQQTA QLVFGIEVV QLVFGIEVV QLVFGIEVV QQTASSSSTI QVARKTGLI QVMPKTGLI QVMPKTGLI QVMPKTGLI QVMPKTGLII QVMPKTGLII QVMPKTGLII QVMPKTGLII QVMPKTGLII QVMPKTGLII QVMPKTGLII SVFAHPRKLI STLVEVTL SSTLVEVTL SVFAHPRKLL SVFAHPRKLL SVFAHPRKLL SVFAHPRKLL SVFAHPRKLL SVFAHPRKLL VMPKTGLLII VMPTGLII VM |

Table VIII A
Mage 2 A02 Supermotif with Binding Data

| | | | | | | 1 | | |
|-------------|----------|-----------------------|--------|--------|--------|--------|--------|------------|
| Sequence | Position | No. of Amino Acids | A*0201 | A*0202 | A*0203 | A*0206 | A*6802 | SEQ ID NO. |
| VVEVVPISHL | 991 | 10 | | | | | | 265 |
| VVPISHLYI | 691 | 6 | | | | | | 566 |
| VVPISHLYIL | 691 | 0 | | | | | | 267 |
| VVPISHLYILV | 691 | = | | | | | | 268 |
| YILVTCLGL | 176 | 6 | | | | | | 269 |
| YLQLVFGI | 157 | ∞ | | | | | | 270 |
| YLOLVFGIEV | 157 | 01 | | | | | | 271 |
| YLÓLVFGIEVV | 157 | = | | | | | | 272 |
| YVKVLHHT | 283 | ∞ | | | | | | 273 |
| YVKVLHHTL | 283 | 6 | | | | | | 274 |
| YVKVLHHTLKI | 283 | = | | | | | | 275 |

Table VIII B
Mage 3 A02 Supermotif with Binding Data

| Amino Acids 8 8 9 10 00007 11 10 00002 9 9 000002 9 10 00002 9 10 00002 9 10 00004 10 10 00004 10 10 00009 10 10 10 00009 10 10 10 10 10 10 10 10 10 10 10 10 10 | Sequence | | A*0201 | A*0202 A*0203 | A*0203 | A*0206 | A*6802 | SEO ID NO. |
|--|----------|-------------|--------|---------------|--------|--------|--------|------------|
| 8 0.0007 | | Amino Acids | | | | | 7000 | |
| 10 | 107 | 8 | | į | | | | 276 |
| 8 0.0001 11 0.0002 10 0.0003 11 0.0004 11 0.0001 10 0.0001 11 0.0001 10 0.0001 11 0.0001 11 0.0001 12 0.0001 13 0.00001 14 0.0001 15 0.0001 16 0.0001 17 0.0001 18 0.0001 19 0.0001 10 0.0001 11 0.00001 11 0.00001 12 0.00001 13 0.00001 14 0.00001 15 0.00001 16 0.00001 17 0.00001 18 0.00001 18 0.00001 19 0.00001 10 0.00001 10 0.00001 | 107 | ₽: | 0.0007 | | | | | 277 |
| 1 | 38 | = ∞ | | | | - | | 976 |
| 1 | 3 % | တ | 0.0001 | | | | | 280 |
| 9 0,0002 10 0,0003 10 0,0004 11 0,0004 10 0,0001 10 0,0001 11 0,0001 12 0,0001 13 0,0001 14 0,0001 15 0,0001 16 0,0001 17 0,0001 18 8 19 0,0001 10 0,0001 11 0,0001 12 0,0001 13 0,0001 14 0,0001 15 0,0001 16 0,0001 17 0,0001 18 0,0001 19 0,0001 10 0,0001 10 0,0001 11 0,0001 12 0,0001 13 0,0001 14 0,0001 | 38 | ν= | | | | | | 281 |
| 9 0.0030 11 0.0024 11 0.0024 11 0.0004 11 0.0004 11 0.0001 12 0.0001 13 0.0001 14 0.0001 15 0.0001 16 0.0001 17 0.0001 18 11 0.0260 19 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 10 0.0001 10 0.0001 10 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 | 207 | :01 | 0.0002 | | | | | 282 |
| 11 0.0024 12 0.0004 13 0.0004 14 0.0001 15 0.0001 16 0.0001 17 0.0001 18 0.0001 18 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 19 0.0001 10 0.0001 10 0.0001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 | 22 | 6 | 0.0030 | | | | | 283 |
| 9 00000 10 00004 11 00004 10 00001 10 00001 10 00001 10 00001 10 00001 11 0.0260 11 0.0260 12 0.0001 13 0.00001 14 0.00001 15 0.00001 16 0.00001 17 0.00001 18 0.00001 19 0.00001 10 0.00001 11 0.0260 12 0.00001 13 0.00001 14 0.00001 15 0.00001 16 0.00001 17 0.00001 18 0.00001 19 0.00001 10 0.00001 10 0.00001 11 0.00001 12 0.00001 | 22 | = | | | | | | 284 |
| 10 | 1 2 | : o | 0.000 | | | | | 286 |
| 10 | 2 | n : | 0.0000 | | | | | 67 |
| 11 0.0024 11 1 | 80. | o ; | 0.0001 | | | | | 987 |
| 10 | 211 | ∞ | | | | | | 287 |
| 1 | 277 | 01 | 0.0024 | | | | | 288 |
| 1 | 77.7 | = | | | | | | 289 |
| 1 | 2, | := | | | | | | 260 |
| 8 0.0001 9 0.0001 9 0.0001 8 0.0001 9 0.0001 9 0.0001 9 0.0001 9 0.0001 9 0.0001 9 0.0001 9 0.0001 9 0.00001 9 0.00001 9 0.00001 9 0.00001 9 0.00001 9 0.00001 9 0.00001 | 9 5 | = : | | | | | | 2.00 |
| 1 | 6 | = | | | | | | 167 |
| 1 | 32 | œ | | | | | | 292 |
| 9 0,0004 8 0,0001 10 0,0001 10 0,0001 10 0,0001 11 0,0260 10 0,0001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 | 215 | | | | | | | 203 |
| 9 0,00004 10 0,0001 10 0,0001 10 0,0001 10 0,0001 11 0,00001 11 0,00001 10 0,0001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 11 0,00001 | C17 | Ξ « | | | | | | |
| 10 | 181 | 6 | 0.0004 | | | | | 294 |
| 8 0,0001 10 0,0001 10 0,0001 10 0,0001 10 0,0001 11 0,0260 8 8 0,0001 11 0,0000 10 0,0001 11 0,0000 10 0,0001 11 0,0001 11 8 8 0,0001 11 8 8 0,0001 11 8 8 0,0001 | [8] | 01 | 0 0001 | | | | | 295 |
| 9 0.0001 8 0.0001 10 0.0001 10 0.0001 11 0.0260 8 8 10 0.0002 11 0.0002 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 | 5 5 |) o | | | | | | 300 |
| 9 0,0001 10 0,0001 10 0,0001 10 0,0001 11 0,0260 11 0,0002 11 0,0001 11 0,0001 11 0,0001 11 0,0001 11 0,0001 11 0,0001 11 0,0001 | 3 : | 5 (| | | | | | 067 |
| 10 | 8 | 5 | 0.0001 | | | | | 297 |
| 8 0.0001 10 0.0001 10 0.0001 11 0.00001 11 0.00002 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 11 0.00001 | 8 | 01 | 0.0001 | | | | | 298 |
| 9 0 00001 8 0 00001 10 0 00001 8 0 00001 11 0 00002 10 0 00001 11 0 0 00001 10 0 0 0001 11 0 0 0 0001 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 77 | ۰ | | | | | | 200 |
| 10 0,0001 8 0,0001 10 0,0001 11 0,0260 8 8 8 0,0002 10 0,0001 11 0,0001 10 0,0001 11 0,0001 11 0,0001 11 0,0001 11 0,0001 11 0,0001 11 0,0001 | \chi | 0 1 | | | | | | 667 |
| 10 0,0001 10 0,0001 10 0,0001 11 0,0260 10 10 0,0001 11 0,0001 10 0,0001 10 0,0001 11 0,0001 10 0,0001 11 0,0001 10 0,0001 11 0,0001 11 0,0001 11 0,0001 | 37 | 5 | 0.0001 | | | | | 300 |
| 8 10 0,0001 10 0,0001 8 11 0,0260 8 10 11 11 8 8 11 0,0002 10 0,0001 11 11 8 8 10 0,0001 10 0,0001 11 11 11 11 11 11 11 11 11 11 11 11 | 37 | 01 | 0000 | | | | | 301 |
| 10 0,0001 8 0,0001 11 0,0260 8 8 10 0,0002 10 0,0001 11 0,0001 10 0,0001 10 0,0001 10 0,0001 11 0,0001 11 0,0001 12 0,0001 13 0,0001 14 0,0001 15 0,0001 16 0,0001 17 0,0001 18 0,0001 19 0,0001 10 0,0001 10 0,0001 10 0,0001 | i 7 | ` o | | | | | | |
| 10 0,0001 10 0,0001 8 8 10 0,0002 10 0,0001 11 0,00001 10 0,0001 11 0,00001 11 0,00001 12 0,0001 13 0,0001 14 0,0001 15 0,0001 16 0,0001 17 0,0001 18 0,0001 19 0,0001 10 0,0001 10 0,0001 10 0,0001 11 0,00001 11 0,00001 12 0,0001 13 0,0001 14 0,0001 15 0,0001 16 0,0001 17 0,0001 18 0,0001 19 0,0001 10 0,0001 1 | 17 | 0 ; | | | | | | 302 |
| 9 0.0001 8 11 0.0260 10 0.0002 10 0.0001 11 0.0001 10 0.0001 10 0.0001 10 0.0001 10 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 | 7 | 01 | 0.0001 | | | | | 303 |
| 10 | 17 | σ | 10000 | | | | | 304 |
| 1 | : : | | 10000 | | | | | , , |
| 8 10 10 10 10 10 10 10 10 10 10 | 2 | 2 | 0.0001 | | | | | 505 |
| 11 | 165 | ∞ | | | | | | 306 |
| 8 10 0.0002 10 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.0001 11 0.00001 11 0.0001 11 | 165 | Ξ | 09000 | | | | | 307 |
| 10 0.0002 10 0.0001 10 0.0001 10 0.0001 8 8 0.0820 0.0500 0.9100 0.0043 1.1000 | 2:- | : • | | | | | | |
| 10 10 10 10 10 10 10 10 10 10 | 2 | 0 | | | | | | 208 |
| 1 1 8 8 8 8 8 8 8 8 | 35 | 01 | | | | | | 309 |
| 8 0.0002 10 0.0001 11 0.0001 10 0.0001 8 8 8 0.0820 0.0500 0.9100 0.0043 1.1000 | 35 | - | | | | | | 310 |
| 8 10 0.0002 10 0.0001 11 0.0001 10 0.0001 8 8 8 9 0.0820 0.0500 0.9100 0.0043 1.1000 | <u>ر</u> | Ξ, | | | | | | OIC. |
| 11 8 10 10 10 10 10 10 10 10 10 10 | 780 | ×0 | | | | | | 311 |
| 8 0.0002 10 0.0001 11 0.0001 10 0.0001 8 8 8 0.0820 0.0500 0.9100 0.0043 1.1000 | 280 | Ξ | | | | | | 312 |
| 8 10 0.0002 10 0.0001 10 0.0001 8 8 8 8 9 0.0820 0.0500 0.9100 0.0043 1.1000 | 007 | : « | | | | | | 210 |
| 10 0.0002 10 0.0001 11 0.0001 10 0.0001 8 8 8 0.0820 0.0500 0.9100 0.0043 1.1000 | 8 | × | | | | | | 313 |
| 10 0.0001 11 0.0001 10 0.0001 8 8 8 0.0820 0.0500 0.0100 0.0043 1.1000 | 168 | 01 | 0.0002 | | | | | 314 |
| 11 9 0.0001 10 0.0001 8 8 8 0.0820 0.0500 0.9100 0.0043 1.1000 | 220 | 01 | 0,0001 | | | | | 315 |
| 9 0.0001 10 0.0001 8 8 8 0.0820 0.0500 0.9100 0.0043 1.1000 | î | 2 = | | | | | | 316 |
| 9 0.0001 10 0.0001 8 8 8 0.0820 0.0500 0.9100 0.0043 1.1000 | 677 | = • | | | | | | 916 |
| 10 0.0001 8 8 9 0.0820 0.0500 0.9100 0.0043 1.1000 | 47 | 5 | 0.0001 | | | | | 317 |
| 8 8 9 0.0820 0.0500 0.9100 0.0043 1.1000 | 47 | 01 | 0.0001 | | | | | 318 |
| 8 8 9 0.0820 0.0500 0.9100 0.0043 1.1000 | 017 | œ | | | | | | 310 |
| 8 9 0.0820 0.0500 0.9100 0.0043 1.1000 | | 0 0 | | | | | | |
| 9 0.0820 0.0500 0.9100 0.0043 1.1000 | 7/1 | ∞ | | | | | | 320 |
| = 6 | 172 | 6 | 0.0820 | 0.0500 | 0.9100 | 0.0043 | 1.1000 | 321 |
| : c | 271 | | | | | | | 322 |
| | 301 | : < | | | | | | 222 |
| | | | | | | | | |

Table VIII B
Mage 3 A02 Supermotif with Binding Data

| SEQ ID NO. | 322 323 323 323 323 323 333 333 333 333 |
|-----------------------|--|
| A*6802 | 0.1500 |
| , A*0206 | 0.0029 |
| A*0203 | 0.1500 |
| A*0202 A*0203 | 0.0140 |
| A*0201 | 0.0001 0.0002 0.0002 0.0003 0.0003 0.0003 0.0001 0.0001 0.0001 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 |
| No. of Amino Acids | 2 & o 2 & o , = & o & o 2 = o = o = c = o & o & o 2 & o 2 = o o & o & o 2 = o = o = o = o = o = o = o = o = o |
| Position | 105 67 67 67 67 67 67 67 67 67 67 67 67 67 6 |
| Sequence | FQAALSRKVA GASSLPTT GASSLPTT GASSLPTT GASSLPTT GASSLPTT GASSLPTT GASSLPTT GASSLPTT GLEARGEA GLEARGEA GLEARGEA GLEARGEA GLIGDNQI IAREGDCA IIAREGDCA IIAREGCLII IMPKAGLLI I |

Table VIII B
Mage 3 A02 Supermotif with Binding Data

| Sequence | Position | No. of Amino Acids | A*0201 | A*0202 | A*0203 | A*0206 | A*6802 | SEQ ID NO. |
|-----------------|------------|-----------------------|--------|--------|--------|--------|--------|------------|
| LIIVLAII | 202 | ∞ (| | | | | | 372 |
| LIGDNOIM | 202 189 | ⊃v ∝ | 0.0008 | | | | | 373 |
| LGDNQIMPKA | 681 | · = | | | | | | 375 |
| LIIVLAI | 201 | ∞ (| | | | | | 376 |
| LIIVLAII | 201 | ب 5 | 0.0001 | | | | | 377 |
| LKYRAREPV | 121 | 2 5 | 0.000 | | | | | 370 |
| LKYRAREPVT | 121 | 2 = | 0000 | | | | | 380 |
| LLKYRAREPV | 120 | = | 0.0001 | | | | | 381 |
| MEVDPIGHL | 991 | 10 | 0.0005 | | | | | 382 |
| JOLVFGIEL | . 28 | 6 : | | | | | | 383 |
| CUVFGIELM | 158 | o : | | | | | | 384 |
| VETSVVKV | 278 | = 0 | 1000 | | | | | 385 |
| VETSYVKVL | 278 | 6 01 | 0.0002 | | | | | 387 |
| LVEVTLGEV | 45 | 6 | 0.0001 | | | | | 388 |
| VEVTLGEVPA | 45 | = | | | | | | 389 |
| LVFGIELM | 160 | 8 | | | | | | 390 |
| LVFGIELMEV | <u>8</u> | 0. | 0.1100 | | | | | 391 |
| VGAQAPA | 2 2 | ∞ | 1000 | | | | | 392 |
| LVGAÇAPAT | 2 7 | o : | 0.0001 | | | | | 393 |
| MVKINGGPHI | 2 5 | | 0,000 | | | | | 394 |
| NOEEEGPST | 68 | ≥ თ | 7000.0 | | | | | 396 |
| NQIMPKAGL | 193 | 6 | | | | | | 397 |
| NQIMPKAGLL | 193 | 01 | | | | | | 398 |
| NQIMPKAGLLI | 193 | = | | | | | | 399 |
| PATEEQEA | 31 | ∞ | | | | | | 400 |
| PATEEQEAA | ₹ ; | 6 (| 0.0001 | | | | | 401 |
| PICHLY IFA | <u> </u> | ъ <u>;</u> | 0.0001 | | | | | 402 |
| HLYIFA! | 1/1 | 2 6 | 0.0003 | | | | | 403 |
| PQCASSLP1 | S % | > ⊆ | | | | | | 404 |
| POGASSE 11 | G Y | 2 = | | | | | | 405 404 |
| POSPOGASSI | 8 6 | | | | | | | 904 |
| PTTMNYPL | 22 | 2 ∞ | | | | | | 408 |
| PVIFSKASSSL | 148 | = | | | | | | 409 |
| PVTKAEML | 129 | & | | | | | | 410 |
| PVTKAEMLGSV | 129 | = | | | | | | 411 |
| QAALSRKV | 901 | ∞ | | | | | | 412 |
| QAALSRKVA | 8 8 | ο: | 0.0001 | | | | | 413 |
| CAMESAN VACE | <u>8</u> g | = = | 10000 | | | | | 414 |
| OAPATEEOEAA | 3 £ | 2 = | 000.0 | | | | | 415 416 |
| QIMPKAGL | 194 | ∞ | | | | | | 417 |
| QIMPKAGLL | 194 | 6 | 0.0001 | | | | | 418 |
| QIMPKAGLLI | 194 | 10 | 9000'0 | | | | | 419 |

Table VIII B
Mage 3 A02 Supermotif with Binding Data

| A*0206 A*6802 SEQ ID NO. | 420 421 423 424 424 426 427 430 431 431 431 433 434 434 434 434 438 438 438 438 | 0.0039 0.1600 441 442 443 444 445 446 447 448 449 450 451 451 451 451 453 |
|--------------------------|--|---|
| A*0203 | | 0009.1 |
| A*0202 | | 0.0320 |
| A*0201 | 0.0010 0.3400 0.0001 0.0002 0.0035 0.0049 | 0.0250 0.0001 0.0009 0.0002 0.0045 |
| No. of Amino Acids | | × |
| Position | 194 159 159 276 276 277 237 237 237 237 237 237 237 237 237 | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |
| Sequence | QIMPKAGLLII QLVFGIELM QLVFGIELMEV QLVFGIELMEV QVPGSDPA RALVETSYVKV RALVETSYVKV RAREPVTKA RAREPVTKA RAREPVTKA RAREPVTKA RAREPVTKA SQLOPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGDPKKLL SILGVFGIEL SLQLVFGIEL STQLVFGIELM SQHCKPEGL STLVEVTL STLVEVTL | ILUEVRAA TLVEYLLGEV TQHFVQENYL VAELVHFLL VAELVHFLLL VIFSKASSSL VLHHMVKI VQENYLEYROV VTKAEMLGSV VTKAEMLGSV VTLGEVPA VTLGEVPA VVGNWQYFFPV WQYFFPVI |

Table IX.a Mage 2 A03 Supermotif with Binding Data

| Position | No. of Amino Acids | A*0301 | A*1101 | A*310i | A*3301 | A*6801 | SEQ ID NO. |
|-----------------------------|-----------------------|--|--|--------|------------------|--------|---------------------------------|
| H 6 | | 0.0009 0.0810 0.0047 | 0.0007 0.1900 0.0018 | 0.0200 | 0.0003 | 0.0280 | 459 460 461 |
| ∞ o = | | -0.0004 0.0021 0.0016 | 0.0005 0.0025 0.0008 | 0.0006 | 0.0190 | 0.0460 | 462 463 464 |
| o- | | 0.0045 0.0011 -0.0009 | 0.0011 | | | | 465 466 467 |
| 0 1 6 | | 0.0002 0.0010 | 0.0002 0.0004 | | | | 468 469 470 |
| ===9 | | 0.0110 0.0780 -0.0002 0.0074 | 0.0170 0.0047 -0.0002 0.0018 | 0.0700 | 0.0074 | 0.0490 | 471 472 473 |
| ? o ⊆ ∞ ∞ ⊆ | | 0.0074 0.00340 0.0053 0.0004 0.0093 | 0.0280 0.0009 0.0100 0.0027 | 0.7700 | 0.8100 | 0.0990 | 475 476 477 478 |
| : ∞ <u>0</u> ∞ <u>0</u> 0 0 | | -0.0009 -0.0004 0.0290 0.0260 0.0027 | -0.0004 0.0001 0.1500 0.0022 | 0.0007 | -0.0009 | 0.0200 | 480 481 482 483 484 |
| ∞==≥∞ | | -0.0009 -0.0009 -0.0003 -0.0009 | -0.0004 0.0120 -0.0002 -0.0004 | 0.0038 | 0.0056 | 0.0220 | 485 486 487 488 489 |
| 0 8 6 3 | | 0.0200 -0.0009 0.0020 | 0.0750 -0.0003 0.0220 | 0.0064 | 0.0003 | 0.0026 | 490 491 492 |
| <u>0</u> | | 0.0002 0.0014 0.1410 0.0140 0.0890 | 0.0002 0.0910 0.0810 0.0550 1.1000 | 0.0130 | 0.0010 0.0370 | 0.0440 | 493 494 495 496 497 |
| 01 | | 0.0033 | 0.0160 | 0.0005 | -0.0009 | 0.0360 | 498 |

| | SEQ ID NO. | 500 500 500 500 500 500 500 500 500 | 509 510 511 | 512 513 514 515 516 517 | 520 522 523 533 | 524 525 526 | 527 528 529 530 |
|---------------------------|-----------------------|---|-------------------------------------|--|---|------------------------------------|--|
| | A*6801 | 0.0022 | -0.0001 | 10000-0- | 0.0200 | 0.0004 | 0980.0 |
| | A*3301 | 0.0004 | -0.0013 | 0.0052 | -0.0009 | 0.0003 | 0.6600 |
| n binding Data | A*3101 | 60000 | -0.0006 | 0.0012 | 0.0007 | 0.0034 | 0.1700 |
| Mage 2 Aug Supermous with | A*1101 | 0.1700 -0.0003 -0.0002 0.0001 0.0011 0.0003 0.0002 | 0.0570 0.0011 0.0037 | 0.0190 0.0021 0.0110 0.0056 -0.0034 0.0030 | 0.1500 0.0022 -0.0002 0.0002 -0.0003 | 0.1100 -0.0003 0.0012 | 0.1400 0.0011 0.0005 0.0061 |
| Mage 2 A | A*0301 | 0.0270 -0.0004 -0.0003 -0.0009 0.00045 0.0011 0.0002 | 0.1300 0.0069 0.0053 | 0.0580 0.0280 0.0200 0.0021 -0.0009 -0.0006 | 0.0290 0.0260 -0.0009 0.0003 | 0.0190 -0.0009 -0.0009 | 0.0003 -0.0002 0.0016 0.0020 |
| | No. of Amino Acids | 6 % 6 I 6 I 2 I 6 S | 2 = 6 ∞ | & <u>0</u> 0 | ∞ <u>2 </u> | 2 ∞ ∞ | o I 8 0 |
| | Position | 277 236 236 224 115 110 102 | 203 204 | 285 202 189 201 120 225 278 | 116 116 266 303 | 276 125 237 | 226 113 227 283 |
| | Sequence | ALVETSYVK DSILGDPK DSILGDPKK ELSYLEVEFEGR ELVHFLLLK ELVHFLLLKYR ESFÇQALSR ESFÇQALSR FLLLKYRAR | GLGDNQIMPK IIVLAIIAR IVLAIIAR | KVLHHWVK LIIVLAIIAR LLGDNQIMPK LLIIVLAIIAR LLLKYRAR LSVLEVFGR | LVHFLLLK LVHFLLLKYR PACYEFLWGPR PLEGRSGHCK PLHEWVLR | RALVETSYVK RAREPVTK SILGDPKK | SVLEVFEGR VAELVHFLLLK VLEVFEGR YVKVLHHMVK |

Table XA
Mage 2. A24 Supermotif Peptides with Binding Data

| Sequence | Position | No. of Amino Acids | A*2401 | SEQ ID NO. |
|----------------------------|------------|-----------------------|--------|------------|
| AISRKMVEL | 108 | 6 | | 531 |
| ALIE ST VN VL CLGLSYDGL | 181 | | | 532 533 |
| CLGLSYDGLL | 181 | 01 | | 534 |
| CYEFLWGPRAL | 268 | = | 0.0004 | 535 |
| DLESEFOAAI | 100 240 | 0. | | 536 |
| DI VOENNI EV | 249 | o <u>S</u> | | 730 |
| EFLWGPRAL | 270 | 2 0 | 0 0006 | 539 |
| EFLWGPRALI | 270 | , <u>2</u> | 0.0097 | 540 |
| EFQAAISRKM | 104 | 10 | 0.0002 | 541 |
| ELSMLEVF | 224 | 80 | | 542 |
| ELVHFLLL | 115 | ∞ | | 543 |
| ELVHFLLLKY | 115 | 10 | | 544 |
| ELST VAVE | 280 | ∞; | | 242 |
| EVECKEDS VF | 677 148 | _ • | | 546 547 |
| EVEVVEICH | 165 | o - | | 247 |
| EVVPISHI. | 891 | <u>-</u> ~ | | 540 |
| EVVPISHLY | 991 | · • | | 550 |
| EVVPISHLYI | 891 | , 0 | | 551 |
| EVVPISHLYIL | 168 | = | | 552 |
| ÉYLQLVFGI | 156 | 6 | 3.5000 | 553 |
| FLWGPRAL | 172 | ∞ | | 554 |
| FLWGPRALI | 271 | 6 | | 555 |
| GIEVVEVVPI | 163 | <u>0</u> | | 556 |
| OLEANGEAL GI EADGEAL | <u></u> | φ; | | 557 |
| OF CANOCAL C | 50 | = 0 | | 928 |
| GLEGGIACTE | 200 | 7 . C | | 929 |
| GLLIIVLAII | 200 | v | | 26. |
| CLSYDGLL | 183 | 2 ∞ | | 295 |
| HLYILVTCL | 174 | o 6 | | \$63 |
| HLYILVTCLGL | 174 | · = | | 564 |
| HTLKIGGEPHI | 289 | = | | 565 |
| IFSKASEY | 150 | ∞ | | 266 |
| IFSKASEYL | 150 | 6 | 0.0230 | 267 |
| IFSKASEYLQL | 150 | = | 0.0950 | 268 |
| IIVLAIIAI | 203 | 6 | | 269 |
| ILVICEGE II VTCI GI SV | // · | ∞ : | | 570 |
| IVLAIIAI | 204 | 2 ∝ | | 575 |
| IWEELSML | 122 |) oo | 0.0007 | 573 |
| IWEELSMLEVF | 221 | ·= | 0.0170 | 574 |
| KIGGEPHI | 292 | ∞ ; | | 575 |
| NIGGERHINY | 767 | 0. | | 576 |

Table XA
Mage 2, A24 Supermotif Peptides with Binding Data

| SEQ ID NO. | 577 578 579 580 582 584 585 586 587 590 591 592 593 | 597 588 589 600 601 603 604 604 604 605 606 610 611 611 611 | 617 619 620 631 |
|-----------------------|--|--|--|
| A*2401 | 0.0005 | 0.1200 0.0086 0.0140 0.0140 0.016 | 0.0150 0.0280 |
| No. of Amino Acids | ∞ o ∞ o o o o o o o o o o o o o o o o o | ~ ♥ ♥ ∞ ∞ 5 ♥ ♥ 5 ≅ 5 ± ∞ ♥ ♥ 5 ± 5 5 | ∞ ⊇ |
| Position | 220 220 112 112 112 198 198 202 201 201 246 246 246 246 | 250 272 273 275 276 277 278 279 279 279 279 279 279 279 279 279 279 | 0 0 0 5 £ £ |
| Sequence | KIWEELSM KWEELSML KWYELVHF KMYELVHFL KMYELVHFLL KMYELVHFLL KTGLLIIVL KTGLLIIVL LIFTSYVKVL LIITSYVKVL LIITSYVKVL LIIVLAII LLIIVLAII LLIIVLAII LLIIVLAII LLIIVLAIIAI | LVQENYLEY LVTCLGLSY LWGPRALI LVILVTCL LVILVTCL LVILVTCLGL MYELVHFL MYELVHFLL MYELVHFLL MYELVHFLL MYELVHFLL PISHLYIL PVIFSKASEY PVIFSKASEY PVIFSKASEY QVMPKTGLL QVMPKTG | SFSTTINY SFSTTINYTLW SFSTTINYTLW SFSTTINYTLW |

Table X.A

| | æI | Mage 2 A24 Supermotif Peptides with Binding Data | inding Data | |
|-------------|----------|--|-------------|------------|
| Sequence | Position | No. of Amino Acids | A*2401 | SEQ ID NO. |
| SVFAHPRKL | 237 | 6 | | 623 |
| SVFAHPRKLL | 237 | . 01 | | 624 |
| SVFAHPRKLLM | 237 | := | | 625 |
| SVLRNCQDF | 138 | 6 | | 626 |
| SVLRNCQDFF | 138 | 10 | | 627 |
| SYPPLHERAL | 300 | 10 | 0.0003 | 628 |
| SYVKVLHHTL | 282 | 10 | 0.1600 | 629 |
| TLKIGGEPHI | 290 | 10 | | 630 |
| TTINYTLW | 73 | 8 | | 631 |
| VFAHPRKL | 238 | 8 | 0.0005 | 632 |
| VFAHPRKLL | 238 | 6 | 9000'0 | 633 |
| VFAHPRKLLM | 238 | 10 | | 634 |
| VFEGREDSVF | 230 | 10 | 0.0004 | 635 |
| VIFSKASEY | 149 | 6 | | 636 |
| VIFSKASEYL | 149 | 10 | | 637 |
| VLHHTLKI | 286 | 8 | | 638 |
| VLRNCQDF | 139 | 80 | | 639 |
| VLRNCQDFF | 139 | 6 | | 640 |
| VMPKTGLL | 195 | 80 | -0.0004 | 641 |
| VMPKTGLLI | 195 | 6 | 0.2300 | 642 |
| VMPKTGLLII | 195 | 01 | 0.0580 | 643 |
| VTCLGLSY | 179 | ∞ | | 644 |
| VTCLGLSYDGL | 179 | = | | 645 |
| VTKAEMLESVL | 130 | = | | 646 |
| VVEVVPISHL | 166 | 10 | | 647 |
| VVEVVPISHLY | 166 | = | | 648 |
| VVPISHLY | 169 | 8 | | 649 |
| VVPISHLYI | 169 | 6 | | 650 |
| VVPISHLYIL | 691 | 10 | | 651 |
| YILVTCLGL | 176 | 6 | | 652 |
| YILVTCLGLSY | 176 | = | | 653 |
| YLQLVFGI | 157 | ∞ | | 654 |
| YVKVLHHTL | 283 | o : | | 655 |
| IANACHUICNI | 797 | | | 929 |

Table X B
Mage 3 A24 Supermotif Peptides with Binding Data

| SEQ ID NO. | 657 658 659 660 661 663 664 665 665 665 667 671 671 671 671 671 672 673 673 674 673 674 675 676 677 677 678 689 689 689 689 690 690 690 690 690 690 690 690 690 69 |
|-----------------------|---|
| A*2401 | 0.0004 0.0006 0.0017 -0.0004 |
| No. of Amino Acids | o = ∞ = o 0 = 2 o ∞ = ∞ ∞ 0 0 ∞ = ∞ o 0 0 = ∞ o o 0 0 ∞ ∞ 0 0 0 0 0 0 0 0 0 0 0 0 0 |
| Position | 100 277 277 179 168 168 168 168 168 168 168 168 168 168 |
| Sequence | ALSRKVAEL ALVETSYVKVL ATCLGLSYDGL CLGLSYDGL EFWGPRAL EFWGPRAL ELWEPRAL ELWEPRAL ELWEPRAL ELWEVDPIGHL ELSVLEVF ELLEVOPIGHL ELVFELLLKY ENLGSYVGNW ETSYVKVL ENLGSYVGNW ETSYVKVL ENLGSYVGNL EVDPIGHL EVGENYLEY GLEARGEALG GLEARGEALG GLEARGEALG GLGDNQIM GLLINVLAI GLLGDNQIM GLLINVLAI GLSSYGGLL HAVIFATCLGL HAVIFATCLGL HAVIFATCLGL HAVIFATCLGL FESKASSSL IFSKASSSL IFSKASSSL |

Table X B

| | SEQ ID NO. | 702 703 706 707 708 707 711 712 713 714 715 716 717 718 719 719 719 719 719 719 719 719 719 719 |
|--|-----------------------|--|
| Sinding Data | A*2401 | 0.4200 0.0500 -0.0004 0.0260 0.0140 0.0480 0.5300 0.0170 0.0270 |
| LADIE O. B. Mage 3 A24 Supermotif Peptides with Binding Data | No. of Amino Acids | ∞ o 2 ∞ 1 ∞ 2 o ∞ o 2 1 o ∞ ∞ ∞ o 12 12 12 ∞ o ∞ 2 o 12 o 2 o ∞ ∞ o 1 ∞ o 0 2 1 ∞ o 0 |
| | Position | 195 195 195 195 195 195 195 195 195 195 |
| - | Sequence | IMPKAGLL IMPKAGLLI IMPKAGLLI IMPKAGLLII IMELSVL IMELSVL IMSGRHII KISGGPHI KISGGPHII KISGGPHII KISGGPHII KVAELVHFL KVAELVHFL KVAELVHFL KVAELVHFL IJIVLAI LLINLAI LNFGIELM LVFGIELM LVFGIELM ROWPKAGLL QIMPKAGLL QIMPKAGLL QIMPKAGLL QIMPKAGLLI QIMPKAGLLI QUMPKAGLLI QUMPKAGLI QUMPK |

Table X B
Mage 3 A24 Supermotif Peptides with Binding Data

| SEQ ID NO. | 747 748 749 750 751 753 754 765 765 765 765 767 777 777 777 777 777 |
|-----------------------|---|
| A*2401 | 0.1200 0.0026 0.0420 0.5900 0.0049 -0.0004 |
| No. of Amino Acids | ≈ 6 5 8 5 1 8 5 1 5 8 8 6 5 1 8 5 6 6 1 8 6 5 5 8 8 6 6 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 |
| Position | 237 237 70 70 70 70 70 157 157 158 138 300 300 300 300 300 300 300 300 300 3 |
| Sequence | QYFFPVIF SILGDPKKL SILGDPKKL SILGDPKKLL SILGDPKKLL SLPTTMNYPLW SLQLVFGIEL SLQLVFGIELM STFPDLESEF STLVPULESEF STLVPULESEF STVGNWQYF SVVGNWQYF SVVGNWQYF SVVGNWQYF SVVGNWQYF SVVGNWQYF VVGNWQYF VYGNWQYF |

Table XI A
Mage 2 BO7 Supermotif Peptides with Binding Data

| | 1 | | | |
|--|---|------------------------------------|--|--|
| Sequence | Position | No. of Amino Acids | B*0702 | SEQ ID NO. |
| APATEEQQTA APEKIWEEL DPACYEFLW EPHISYPPL EPHISYPPL EPYTKAEM EPYTKAEM EPYTKAEM EPYTKAEM FPDLESEFQA FPNFSKAEV GPRALIETSY GPRALIETSY GPRALIETSY GPRALIETSY GPRALIETSY FPNFSCALIII MPKTGLLII MPKTGLII MPKTG | 30 216 255 255 255 255 256 274 274 274 274 274 276 276 277 277 276 277 277 277 277 277 | 22∞00∞0∞2=∞=2=∞2=∞∞02=∞=∞0≈=o=∞02∞ | 0.0002 0.0001 0.0001 0.0001 0.0001 0.0002 0.0003 | 777 786 787 787 788 788 799 799 800 800 800 800 800 800 800 800 800 8 |
| YPPLHEKAL | 105 | 6 | 0.2700 | 812 |

| 20 ∞ 0 ∞ 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |
|---|
| ² ∞∞∞∞055±∞∞∞∞5±∞∞05±∞∞∞5±∞∞±±∞∞± |
| 0 ∞ 0 5 5 ± 0 ∞ 0 ∞ 5 ± ∞ 0 5 ± ∞ 0 5 ∞ 0 5 ± ∞ 0 ± ± ∞ 0 ± 0 ± 0 ± 0 ± 0 ± 0 ± 0 ± |
| ∞ ♥ 5 5 ± ♥ ♥ ♥ 5 ± ♥ \$ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ ₹ |
| |
| 55=°∞°°5=∞°°5=∞°°5=∞°°5=∞°°5=∞°°5=∞°°5= |
| 5 = o ∞ o ∞ 5 = ∞ o 5 = ∞ o 5 = ∞ o 5 = ∞ o = ∞ o = ∞ |
| : □ ♥ ♥ ♥ ♥ □ □ ♥ ♥ ♥ □ □ ♥ ■ □ □ ♥ ■ □ □ ♥ □ ■ □ □ ■ □ □ ■ □ □ ■ □ □ □ ■ □ □ □ ■ □ □ □ ■ □ □ □ ■ □ □ □ ■ □ □ □ □ ■ □ □ □ □ □ □ ■ □ □ □ □ ■ □ □ □ ■ □ |
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| · · O I · & & O I · & & A · D · & & O I · & & I I · & & A I · · · · · · · · · · · · · · · · · · |
| :=∞⊙⊆=∞∞⊙⊆∞∞==∞∞== |
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| : ∞ ∞ = = ∞ o = o |
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| Table XII A | Mage 2 B27 Supermotif Pentides |
|-------------|--------------------------------|
| | |

| | Mage 7 BZ/ Supermotif Peptides | | |
|----------------------------|--------------------------------|-----------------------|--------------------|
| Sequence | Position | No. of Amino Acids | SEQ ID NO. |
| AHPKKLLM AHPKI I MODI | 240 | 8 - | 851 |
| AREPVTKAEM | 126 | 01 | 853 |
| AREPVTKAEML | 126 | 2 = | 854 |
| ARGEALGL | 18 | ∵∞ | 855 |
| EKIWEELSM | 219 | 6 | 856 |
| EKIWEELSML | 219 | 10 | 857 |
| LKIGGEPHI | 291 | 6 | 858 |
| LKIGGEPHISY | 291 | = | 826 |
| LRNCQDFF | 140 | 8 | 980 |
| LRNCQDFFPVI | 140 | = | 861 |
| PHISYPPL | 297 | 8 | 862 |
| PHSPQGASSF | 62 | 10 | 863 |
| PKTGLLII | 197 | œ | 864 |
| PKTGLLIIVL | 197 | 10 | 865 |
| PRALIETSY | 275 | 6 | 998 |
| PRKLLMQDL | 242 | 6 | 867 |
| PRMFPDLESEF | 95 | = | 898 |
| QHCKPEEGL | 8 | 6 | 698 |
| RKLLMQDL | 243 | 8 | 870 |
| RKMVELVHF | Ξ | 6 | 871 |
| RKMVELVHFL | Ξ | 10 | 872 |
| RKMVELVHFLL | Ξ | = | 873 |
| SHLYILVTCL | 173 | 10 | 874 |
| SKASEYLQL | 152 | 6 | 875 |
| SKASEYLQLVF | 152 | = | 876 |
| SRKMVELVHF | 110 | 10 | 877 |
| SRKMVELVHFL | 110 | = | 878 |
| TKAEMLESVL | 131 | 10 | 628 |
| VHFLLLKY | 117 | ∞ (| 880 |
| VK VLHHILKI VK VLHHTLKI | 284 284 | 8 CT | - 88 883 883 |
| | | 2 | |

| F4 | |
|----|--|
|----|--|

| | <u> 1adie Au B</u> Mage 3 B27 Supermotif Peptides | All B ermotif Peptides | |
|--|---|--|--|
| Sequence | Position | No. of Amino Acids | SEQ ID NO. |
| KREPUTKAEM KREPUTKAEML KRGEALGL KKWEELSVL HISTOL HISTOPPL HISTOPLHEW KAGLLII KAGLLII KKAGLLIIIVL KKAGLLIIIVL KKAGLLIIIVL KKAGLLIIIVL KKAGLUIIVL KKVAELVHF RAL VETSY HICYOBNY HISTOPPL H | 126 126 18 173 297 297 297 297 298 8 8 248 248 248 111 111 110 110 110 291 | 0=∞00∞∞=∞00000000000000000000000000000 | 883 884 885 887 887 887 890 891 892 893 894 895 896 900 900 905 906 906 |
| | | | |

Table XIII A

Table XIIIA
Mage 2 B58 Supermotif Peptides

| | SEQ ID NO. | 956 957 958 969 960 960 972 973 973 974 975 975 976 977 977 978 978 978 978 978 978 978 978 |
|--------------------------------|-----------------------|--|
| if Peptides | No. of Amino Acids | 0 = ∞ ∞ 0 = 0 = ∞ 0 = 0 = ∞ 0 0 ∞ = ∞ 0 ∞ 0 |
| Mage 2 B58 Supermotif Peptides | Position | 198 266 106 106 37 37 37 40 69 69 69 69 69 69 77 72 73 73 73 73 73 73 73 73 73 |
| - | Sequence | KTGLLIIVL KTGLLIIVL KTGLLIIVLI PACYEFLW QAAISRKMV QAAISRKMVEL QTASSSSTL QTASSSSTL QTASSSSTLV QTASSSSTLV RALIETSYV SSFSTTINYT SSSFSTLV SSSFTLV SSSTLV SSSTLV SSSTLV SSSTLV SSSTLV SSSTLV STTINYTL STTINYTL TASSSSTLV TASSSTLV TASSTLV TASSSTLV T |

Table XIII B

| L. L | Sequence | Position | No. of | SEQ ID NO. |
|--|-----------------------|----------|-------------|------------|
| 107 107 107 10 38 8 8 8 8 8 11 68 8 8 8 11 154 9 8 10 179 8 8 11 179 9 8 11 170 170 170 170 170 170 170 170 170 170 170 170 170 170 170 | | | Amino Acids | |
| 197 198 198 198 199 199 199 199 199 | AALSRKVAEL | 201 | 10 | 066 |
| 3.8 5.8 5.8 5.8 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9 | (VAELV TI | 107 | _ • | 166 |
| 6.6 6.8 6.8 1.54 1.5 | AASSSTLV AASSSSTLV | တို့ ထို | 8 6 | 993 |
| 6.8 6.8 154 154 154 154 154 154 154 154 | TLVEV | 38 | = | 994 |
| 154 154 154 154 154 154 154 154 | TM | 89 | 80 | 995 |
| 134 4 3 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | TMNY | 89 | 0, | 966 |
| 179 179 179 179 179 179 179 179 | . ve | 154 | ∞ 0 | 166 |
| 39 | LVFGI | 154 | | 966 |
| 39 179 179 179 179 179 179 170 170 170 170 170 170 170 170 170 170 | ; :>1 | 39 | : ∞ | 0001 |
| 179 8 215 216 236 236 236 37 37 37 37 37 37 37 37 37 37 | LVEV | 39 | 01 | 1001 |
| 215 215 216 236 236 236 37 37 37 37 37 37 37 37 37 37 | SY | 179 | ∞ | 1002 |
| 236 236 236 236 237 37 37 37 37 37 37 37 37 37 | SYDGL | 179 | = | 1003 |
| 236 236 236 236 236 236 237 37 17 17 17 17 18 280 280 280 280 280 280 280 280 280 28 | M. | 215 | ∞ | 1004 |
| 236 236 236 236 37 17 17 17 17 18 28 28 28 28 28 28 28 28 28 28 29 29 29 29 29 29 29 29 29 29 29 29 29 | IWEEL | 215 | = | 1005 |
| 236 37 37 37 10 10 280 280 280 151 151 151 151 162 280 178 88 88 178 187 197 198 198 198 198 198 198 | PKKL | 236 | 10 | 9001 |
| 37 17 18 19 280 280 280 280 178 188 181 181 181 182 283 263 263 263 263 263 263 263 279 299 299 299 299 299 299 299 | PKKLL | 236 | | 1001 |
| 177 177 100 178 178 179 170 188 178 179 170 189 179 170 189 189 189 189 199 170 189 189 199 189 199 189 189 189 189 189 | STL | 37 | 6 : | 1008 |
| 17 17 280 280 280 280 280 280 280 280 280 280 | STLV | 37 | 01 | 6001 |
| 280 280 280 178 151 151 151 151 151 151 151 15 | Ter | | σ; | 0101 |
| 280 280 280 280 280 280 178 151 151 151 151 263 263 263 263 293 299 299 299 299 299 299 299 299 29 | ן. פור י | <u> </u> | <u> </u> | 100 |
| 280 178 151 151 151 151 167 67 67 67 67 67 67 67 67 67 | VI. | 102 | ∞ ∞ | 2012 |
| 178 178 9 9 15 15 15 16 16 16 16 16 | VLHHM | 280 | > <u>_</u> | 4101 |
| 151 151 160 161 | LSY | 178 | . 6 | 1015 |
| 151 151 151 151 151 152 263 263 263 263 263 263 263 26 | SL | 151 | 8 | 1016 |
| 151 | SLQL | 151 | 01 | 1017 |
| 67 67 9 263 263 10 263 263 10 137 11 137 11 299 9 299 10 299 10 132 8 198 8 198 8 | SLQLV | 151 | = | 1018 |
| 263 263 11 12 12 13 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15 | ДW | 29 | 6 | 1019 |
| 263 263 263 263 263 137 137 137 229 299 299 299 10 132 132 198 198 | TTMNY | 29 | = | 1020 |
| 263 263 137 137 137 229 229 229 229 132 132 132 133 143 158 158 169 | YEF | 263 | 6 | 1021 |
| 263 137 137 137 137 130 299 299 10 299 11 132 8 132 9 9 198 198 198 | YEFL | 263 | 01 | 1022 |
| 137 10 137 11 137 10 299 9 299 10 132 8 132 8 198 8 | YEFLW | 263 | Ξ, | 1023 |
| 137 11 293 299 9 299 10 299 11 132 8 132 8 198 8 198 8 | WQY 1.00√ | 137 | ٠. | 1024 |
| 293 299 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | NOYF MOXEE | 13/ | 2 - | 5701 |
| WV 299 9 9 10 10 10 10 10 10 10 10 10 10 10 10 10 | YWCIFF SX | 13/ | <u> </u> | 1028 |
| WV 299 10 WV 299 10 V 132 8 VV 132 9 198 8 | EW | 253 | ۰ ٥ | 1201 |
| WVL 299 11 132 8 8 8 9 9 9 9 9 9 9 | FWV | 566 | \ <u>0</u> | 6201 |
| VV (32 8 9 9 9 198 8 8 9 9 9 9 9 9 9 9 9 9 9 9 | EWVL | 299 | ? = | 1030 |
| VV 132 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | SV | 132 | 88 | 1031 |
| 198 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | SSVV | 132 | 6 | 1032 |
| 10 861 | > 5 | 86.0 | ∞ c | 1033 |
| | VI.AI | 861 | · = | 1035 |

| Collience | Position | No of | SEO ID NO |
|-----------------|-----------|-------------|-----------|
| sedneuce | I OSITION | Amino Acids | 35 JU 10 |
| KASSSLQL | 153 | 8 | 1036 |
| KASSSLÓLV | 153 | 6 | 1037 |
| KASSSLQLVF | 153 | 01 | 1038 |
| LSRKVAEL | 601 | ∞ | 1039 |
| LSRKVAELV | 109 | 6 | 1040 |
| LSRKVAELVHF | 109 | = | 1041 |
| LTQHFVQENY | 246 | 01 | 1042 |
| LTQHFVQENYL | 246 | = | 1043 |
| PACYEFLW | 592 | 8 | 1044 |
| PSTFPDLESEF | 95 | = | 1045 |
| PTTMNYPL | 72 | 8 | 1046 |
| PTTMNYPLW | 72 | 6 | 1047 |
| QAALSRKV | 106 | ∞ | 1048 |
| QAALSRKVAEL | 106 | = | 1049 |
| QSPQGASSL | 63 | 6 | 1050 |
| RALVETSY | 276 | ∞ | 1051 |
| RALVETSYV | 276 | 6 | 1052 |
| RALVETSYVKV | 276 | = | 1053 |
| RAREPVTKAEM | 125 | = ; | 1054 |
| RSQHCKPEEGL | 9 | _ (| 1055 |
| SSLPTTMNY | 69 | ς: | 1056 |
| SSLPITMNYPL | 69 | = ‹ | /501 |
| SSLQLVFGI | 96 | 5 | 8501 |
| SSLQLVFGIEL | 156 | _ | 6501 |
| SSSLQLVF | 155 | ∞ ; | 0901 |
| SSSLQLVFGI | 155 | 0, | 1901 |
| SSSSTLVEV | 40 | 6 | 1062 |
| SSSSTLVEVTL | 40 | | 1063 |
| SSSTLVEV | 41 | ∞ | 1064 |
| SSSTLVEVTL | 41 | 01 | 1065 |
| SSTLVEVTL | 42 | 6 | 1066 |
| STFPDLESEF | % | 10 | 1067 |
| STLVEVTL | 43 | ∞ | 1068 |
| STLVEVTLGEV | 43 | = | 1069 |
| TSYVKVLHHM | 281 | 01 | 1070 |
| TSYVKVLHHMV | 281 | = | 101 |
| TTMNYPLW | 73 | ∞ | 1072 |
| VAELVHFL | 113 | ∞ · | 1073 |
| VAELVHFLL | 113 | 6 | 1074 |
| VAELVHFLLL | 113 | 01 | 1075 |
| VTKAEMLGSV | 130 | 01 | 9.01 |
| 77.50 EVE VILLE | | | |

| Table XIV A | Mage 2 B62 Supermotif Peptides |
|-------------|--------------------------------|
|-------------|--------------------------------|

| | SEQ ID NO. | 1078 1080 1080 1083 1083 1084 1085 1095 1096 1097 1100 1100 1110 1110 1110 1110 1110 | C711 |
|--------------------------------|-----------------------|--|------------|
| rmotif Peptides | No. of Amino Acids | Ç∞2∞020∞2∞2≡∞020∞=02∞2∞0002==02∞∞∞∞2∞∞2∞∞0∞0∞0∞∞ | 7 |
| Mage 2 B62 Supermotif Peptides | Position | 2777 2777 2777 2777 2777 2777 2777 277 | 107 |
| - | Sequence | ALIETSYV ALIETSYV ALIETSYV CQDFFPVI CQDFFPVI CQDFFPVI CQDFFPVI CQDFFPVI CQDFFPVI CQDFFPVI ELSMLEVF ELVHFLLLKY ELSMLEVF ELVHFLLKY ELVHFLLKY ELVHFLLKY ELVHFLLKY ELVHFLLKY ELVHFLLKY ELVHFLLKY ELVHFLLKY ELVHSHLYI FPULESEF FPVIFSKASEY FQAAISRKM GQAAISRKM GLGDNQV GLLGDNQV GLLGDNQV GLLGDNQV GLLGDNQV GLLGDNQV GLLGDNQV GLLGDNQV KRWELSNY KRGGEPHISY KRGGEPHISY KRWELSNLEV KRWELSNLEV KRWELSNLEV KRWELSNLEV KRWELSNLEV KRWELSNLEV LIFTSYVKV LIINTAII LITTAII LITTAIIAI | בדון גראוו |

| | SEQ ID NO. | 1123 1124 1127 1128 1133 1133 1133 1133 1134 1135 1136 1137 1138 1138 1138 1138 1138 1138 1138 |
|--|-----------------------|--|
| Peptides | No. of Amino Acids | |
| <u>Table XIV A</u> Mage 2 B62 Supermotif Peptides | Position | 201 245 256 256 257 258 258 258 258 258 258 258 258 258 258 |
| | Sequence | LLINYAIIAI LLKYRAREPV LLKYRAREPV LLKYRAREPV LLMQDLVQENY LMQDLVQENY LQLVFGIEVV LVEVTLGEV LVFGIEVV LVFGIEVV LVFGIEVV LVFGIEVV LVFGIEVV LVFGIEVV LVFGIEVV LVGIEVVEV LVFGIEVV LVGIEVVEV LVGIEVVEV LVGIEVVEV LVGIEVVEV LVGEEGRRM MPKTGLLII MVQEEGRRM VQEEGRRM VQEEGRRM VQEEGRRM VQEEGRRM VQEEGRRM VQEEGRRM VQVASSSSTLV QVMPKTGLLII QVGSDPACY SVLANCQDFF TLKUCQDFF VLRNCQDFF VLRNCQDFF |

| | <u>Table XIV A</u> Mage 2 B62 Supermotif Peptides |
|--|--|
|--|--|

| Position | No. of Amino Acids | SEQ ID NO. |
|----------|-----------------------|------------|
| 195 | 6 | 1170 |
| 195 | 10 | 1171 |
| 195 | = | 1172 |
| 761 | 6 | 1173 |
| 761 | = | 1174 |
| 170 | 8 | 1175 |
| 170 | 01 | 1176 |
| 251 | 8 | 1177 |
| 251 | = | 1178 |
| 991 | = | 1179 |
| 169 | ∞ | 1180 |
| 169 | 6 | 1181 |
| 691 | = | 1182 |
| 176 | = | 1183 |
| 157 | 8 | 1184 |
| 157 | 01 | 1185 |
| 157 | = | 1186 |
| 283 | = | 1187 |

| | Table XIV B Mage 3 B62 Supermotif Peptides | | |
|---|--|-----------------------|-------------|
| Sequence | Position | No. of Amino Acids | SEQ ID NO |
| CVAFIV | 108 | 01 | 901. |
| rsyv | 277 | 2 ∞ | 8 - - |
| LSYVKV | 277 | 10 | 81 |
| YEFLW | 265 | 6 | 1611 |
| ILY1 II XIE | 0/1 | ∞ (| 1192 |
| LTIP ITTOHE | 241 | ν . | <u> </u> |
| LLTOHFV | 241 | 2 = | <u> </u> |
| VDPI | 165 | - ∞ | 1 2 2 |
| EVF | 224 | 8 | 1197 |
| FLLLKY | 115 | 10 | 1198 |
| W C C C C C C C C C C C C C C C C C C C | 134 | 0, | 661 |
| ×55M | 871 | ∞ ⟨ | 1200 |
| Z INC | 901 | ν <u>-</u> | 1201 |
| JIX IND | 97 | 2 = | 7071 |
| REDSI | 229 | | 2071 |
| PRALV | 271 | 2 σ | 1204 |
| SEF | | \ oc | 5021 |
| LSRKV | 105 | . 6 | 1207 |
| 4YLEY | 250 | 6 | 1208 |
| EVDPI | 163 | 10 | 1209 |
| IÒNO | 188 | ∞ : | 1210 |
| SNOIM 1 A I | 88.7 | 6 | 1211 |
| /LAI | 700 | ο · | 1212 |
| VETSY | 200 | 0 0 | 1213 |
| VETSYV | 274 | 2 = | 1215 |
| PLHEW | 298 | 01 | 1216 |
| PLHEWV | 298 | = | 1217 |
| ISGGPHI | 289 | = | 1218 |
| יטבורן סרו זו | 261 | б : | 1219 |
| GELII | | 0. | 220 |
| PH! | 293 | = ∞ | 177 |
| PHISY | | , <u>o</u> | 1223 |
| ırsv | 220 | : ∞ | 1224 |
| LSVLEV | 220 | = | 1225 |
| OHFV Street | 244 | ∞ : | 1226 |
| JANKI | 112 | ∞ | 1227 |
| | 202 | 7 ∖∞ | 877 |
| WION | 189 | > ∞ | 1230 |
| AI | 201 | ∞ | 1231 |
| Ali A B E B V | 201 | 6 | 1232 |
| CARETY | 171 | 0 | 1233 |

| | SEQ ID NO. | 1234 1235 1236 1237 1238 1239 1240 1240 1241 1241 1244 1244 1244 1244 |
|--|-----------------------|--|
| tides | No. of Amino Acids | |
| <u> Table XIV B</u> <u>Mage 3 B62 Supermotif Peptides</u> | Position | 245 245 246 247 248 258 259 260 260 270 270 270 270 270 270 270 27 |
| | Sequence | LLLKYRAREPV LLTQHFVQENY LMEVDPIGHLY LYEVTGELM LVEYTGELM LVFGIELM MPKAGLLII QUMPKAGLLII QUMPKAGLII QUMPKAGLI |

| | | SEQ ID NO. | | 1280 | 1281 | 1282 | 1283 | 1284 | 1285 | 1286 |
|-----------|----------------------|-----------------------|-----------|--------------|-----------|------------|-----------|------------|------|-------------------|
| 8 | otif Peptides | No. of Amino Acids | | 6 | = | ∞ | ∞ | ∞ | 6 | _ |
| Table XIV | Mage 3 B62 Supermoti | Position | | 143 | 9/1 | // | 301 | 283 | 283 | 783 |
| | | Sequence | WOVEEDVIE | VIEATCI OF S | VPI WENCE | VPPI HEWAY | VVVVI UUN | VVVVI UUNV | | I AVA FIIIIMIA VI |

| Table XV A | lage 2 A01 Motif Peptides with Binding Data |
|-------------------|---|
| | Mage 2 |

| nding Data | A*0101 SEQ ID NO. | 0.1700 1287 0.0047 1288 -0.0021 1289 0.0023 1290 0.0450 1291 1.5000 1291 -0.0021 1293 -0.0006 1294 -0.0021 1295 -0.0021 1296 -0.0021 1296 -0.0021 1296 -0.0021 1296 |
|---|-----------------------|---|
| Table XV AMage 2 A01 Motif Peptides with Binding Data | No. of Amino Acids | <u></u> |
| B | Position | 68 67 294 150 150 247 247 275 275 69 69 179 166 |
| | Sequence | ASSESTTINY GASSESTTINY GGEPHISY IFSKASEY LIMQDLVQENY MQDLVQENY PGSDPACY PRALIETSY SFSTTINY SFSTTINY VQENYLEY VQENYLEY |

| Table XV B | e 3 A01 Motif Peptides with Binding Data |
|------------|--|
| | Mage 3 A0 |

| | Mage 3 AO | Table XV B Mage 3 A01 Motif Peptides with Binding Data | | |
|----------------------|-----------|---|---------|------------|
| Sequence | Position | No. of Amino Acids | A*0101 | SEQ ID NO. |
| A S S 1 DTTP A CALLY | | | | |
| ASSERTIMINT | 89 | 10 | 2.6000 | 1300 |
| AICLOLSY | 179 | ∞ | 0.1100 | 1301 |
| EVDPIGHLY | | 6 | 18.0000 | 1302 |
| GASSLPLIMNY | 29 | = | 0.0390 | 1303 |
| CONNCINCT | 137 | 6 | 0.0500 | 1304 |
| IFATCLGLSY | 177 | 01 | 00000 | 100 |
| ISGGPHISY | 293 | 2 0 | 0.0020 | 1303 |
| KISGCPHISY | 202 | | 0.03/0 | 1306 |
| LGSVVGNWOX | 27.7 | 0.7 | 0.0011 | 1307 |
| I MEVIDECHI V | 130 | 01 | 0.0020 | 1308 |
| LINEVOLUCIO | 96 | = | 7.5000 | 1309 |
| DOCUBACY | 246 | 01 | 0.2600 | 1310 |
| DBA1 VETSV | 797 | ∞ | -0.0021 | 1311 |
| CCI PITTO DIV | Ç/7 | 6 | 0.0011 | 1312 |
| Solit I Mily I | 69 | 6 | 0.0550 | 1313 |
| MINTPLWS(SY | 74 | = | 0.0830 | 1314 |
| VÇENTLET | 251 | ∞ | -0.0021 | 1315 |
| | | | | |
| | | | | |

| ing Data | A*0301 SEQ ID NO. | 0.0003 1316 0.0002 1317 0.0009 1320 1321 0.0003 1324 0.0001 1328 0.0002 1328 0.0004 1339 0.0004 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1338 0.0007 1349 0.0007 1359 0.0007 1359 0.0007 1359 0.0007 1359 0.0007 1359 0.0007 1359 0.0007 1359 0.0007 1359 0.0007 1359 0.0007 1359 |
|--|-----------------------|---|
| Table XVI A Mage 2 A03 Motif Peptides with Binding Data | No. of Amino Acids | o 2 = 8 = 2 = o = o o 2 8 o 2 8 o 5 = s o 8 2 o 8 2 o 6 8 8 o o o o 8 o 2 8 = o 2 = 8 = 2 = 6 = 5 = 6 = 5 = 6 = 6 = 6 = 6 = 6 = 6 |
| | Position | 267 55 55 55 55 55 55 55 55 55 55 55 55 55 |
| | Sequence | AADSPSPPH ACYEFLWGPR ACYEFLWGPR ACYEFLWGPR AIRGDCAPEEK AIRGDCAPEEK AIRGDCAPEEK AIRGOCAPEEK AIRGOCAPEEK AIRGOCAPEEK ALGLVGAQA ALGLVGAQA ALGLVGAQA DLESEFQA DLESEFQA DLESEFQA DLVQENYLEYR DSVFAHPR EALGLVGA EALGLVGA EALGLVGA ECLVGAQA ELSEFQAAISR EGREDSVF ECLVGPRA ECREDSVF ECREDSVF ELVHFLLK ECLVF ELVHFLLK ELVHFLLK ELVHFLLK ELVHFLLK ELVHFLLK ELVHFLLK ELVHFLLK ESSEFQAAISR ESSEFQAAISR ESSEFQAAISR ESSEFQAAISR ESSEFQAAISR ESSEFQAAISR ESSEFQAAISR ELVHFLLK ELVHFLLK ELVHFLLK ELVHFLLK ELVHFLLK ESSEFQAAISR |

| | SEQ ID NO. | 1363 | 1363 | 1364 | 1365 | 1366 | 1367 | 1368 | 1369 | 1370 | 1371 | 1372 | 1373 | 1374 | 1375 | 1376 | 1377 | 13/8 | 13/9 | 1361 | 1381 | 1382 | 1383 | 1385 | 1386 | 1387 | 1388 | 1389 | 1390 | 1391 | 1392 | 1393 | 1395 | 1396 | 1397 | 1398 | 1399 | 1400 | 1401 | 1402 | 1404 | 1405 | 1406 | 140/ |
|---|-----------------------|-----------|--------------------------|------------|------------|----------|-----------|----------|----------|-------------|-------------|----------|----------|----------|----------|-------------|----------|-------------|-----------|------------|--------------|----------------|---------|------------|------------|----------|------------|-------------|-----------|------------|----------|-----------|----------|-----------|------------|------------|-------------|-----------|-----------|--------------|------------|----------|------------|----------|
| g Data | A*0301 | 0 0003 | 0.0003 | 20000 | 20000 | 1000:0 | 00003 | | | 0110 | | | | | | 0.0780 | | 000 | 0.0003 | 60000 | -0.0002 | 6000.0 | | 91000 | 0.0014 | | 0.0074 | | 0.0002 | | | | | | 0.0036 | 0.0002 | | 0.0340 | 60000 | 0.0002 | | | 2000 | 6500.0 |
| Table XVI A Mage 2 A03 Motif Peptides with Binding Data | No. of Amino Acids | ď | ^ | 2 = | 2 α | Λ ∝ | ာဇာ | \ | . o | `= | == | : ∞ | 8 | 8 | 8 | = (| ∞ ; | = (| 50 | ^ : | _ : |) : | = ∞ | ~ ~ | 01 | 2 00 | . 01 | = | 6 | 01 | ∞ ‹ | × | ~ 0 | `∞ | 01 | 10 | = | σ: | 2 : | 2 5 | 2 2 | ∞ | 0° | ∞ |
| | Position | 47 | 4 4 | | 891 | 146 | 146 | 61 | 911 | 12 | | 213 | 161 | 294 | 15 | 880 | 200 | 700 | 24 | 507 86 | 800 | n 0 | 218 | 87 | 8 = = | 298 | 298 | 298 | 63 | 289 | 507 | 303 | 208 | 203 | 171 | 601 | 109 | 299 | 299 | 152 | 292 | 112 | 861 | C87 |
| | Sequence | EVTIGEVPA | EVILCEVIA FVTI GEVPAA | FVVEVVPISH | EVVPISHI V | FFPVIFSK | FFPVIESKA | FILKYRA | FLLKYRAR | FSTTINYTIME | GASSFSTTINY | GDCAPEEK | GDNQVMPK | GGEPHISY | GLEARGEA | GLLGDNQVMPK | GLLIIVLA | GLLIFVLAIIA | GLVGAQAPA | CSDFACTEF | USSINGEEEURK | UCK PEECLEA | HEITKVR | HELLKYRA | HFLLLKYRAR | HISYPPLH | HISYPPLHER | HISYPPLHERA | HSPQGASSF | HTLKIGGEPH | IAIEGDCA | ICCEPHISY | HAIEGDCA | IIVLAIIA | ILVTCLGLSY | ISRKMVELVH | ISRKMVELVHF | ISYPPLHER | ISTPLHERA | KASEVI OI VE | KIGGEPHISY | KMVELVHF | KTGLLIIVLA | KVLHHILK |

| Position Amno Acids Av301 SEQ 206 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | No. of Armino Acids 1 | | | <u>Table XVI A</u> Mage 2 A03 Motif Peptides with Binding Data | ata | |
|--|--|-----------------------|------------|---|---------|--------------|
| 206 11 0.0002 23 8 0.0003 278 8 0.0004 278 8 0.0004 278 10 0.0004 200 11 0.0004 201 10 0.0004 202 9 0.0004 245 11 0.0004 245 11 0.0004 245 11 0.0004 246 10 0.0004 247 11 0.0004 248 11 0.0004 249 0.0004 0.0004 250 9 0.0002 250 9 0.0002 270 9 0.0002 271 11 0.0002 272 11 0.0002 273 11 0.0002 274 11 0.0002 275 10 0.0002 28 0.0002 0.0002 29 0.0002 0.0002 20 0.0002 0.0002 | 206 11 0.0002 23 8 0.0003 278 8 0.0004 278 8 0.0009 207 9 0.0009 201 10 0.0009 202 11 0.0009 212 10 0.0009 245 11 0.0009 246 11 0.0009 247 11 0.0009 250 10 0.0009 251 11 0.0009 250 9 0.0002 250 9 0.0002 250 9 0.0002 250 9 0.0002 250 9 0.0002 260 9 0.0002 270 8 0.0002 271 11 0.0002 282 8 0.0003 283 10 0.0003 284 10 0.0003 285 10 0.0003 286 8 0.0003 286 8 0.0003 287 10 0.0003 288 10 0.0003 290 0.0003 0.0003 | sequence | Position | No. of Amino Acids | | SEQ ID NO. |
| 233 8 8 0 00002 223 8 8 8 0 00002 223 8 8 8 0 00004 223 8 8 8 0 00004 2245 11 10 0 0003 2245 11 10 0 00004 225 11 10 0 00004 225 11 10 0 00004 225 11 10 0 00004 226 11 10 0 000004 227 11 10 0 00000 228 8 0 00000 229 9 9 9 0 000002 220 22 8 8 0 000003 220 22 8 8 0 000003 220 22 8 8 0 000003 220 22 8 8 0 000003 220 22 8 8 0 000003 220 22 8 8 0 000003 220 23 8 0 000003 221 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 233 8 8 0 00002 278 8 8 8 0 00003 278 8 8 8 0 00003 278 8 8 8 0 00003 279 9 10 00003 270 9 11 0 00003 270 9 11 0 00003 270 11 | AllAlEGDCA | 206 | =: | | 1408 |
| 23 9 0,0003 278 8 0,0003 29 0,0003 0,0003 245 11 0,0003 245 11 0,0003 245 11 0,0003 245 11 0,0003 246 11 0,0003 247 11 0,0004 248 0,0004 0,0004 249 0,0004 0,0002 250 11 0,0002 270 8 0,0002 271 11 0,0002 272 8 0,0003 273 11 0,0003 274 11 0,0003 275 11 0,0003 276 11 0,0003 277 11 0,0003 28 0,0003 0,0003 29 0,0003 0,0003 20 11 0,0003 20 11 0,0003 20 11 0,0003 20 11 0,0003 <td>23 3 0.0003 273 8 0.0003 273 10 0.0004 273 11 0.0004 274 11 0.0009 275 10 0.0009 275 11 0.0009 275 11 0.0009 276 11 0.0009 277 8 0.0003 277 8 0.0003 277 8 0.0003 277 8 0.0003 278 10 0.0003 282 10 0.0003 282 10 0.0003 283 10 0.0003 284 10 0.0003 285 10 0.0003 286 8 0.0003 287 10 0.0003 288 0.0003 0.0003 290 0.0003 0.0003 20 0.0003 0.0003 20 0.0003 0.0003 20 0.0003 0.0003 <td>GDNOVMPK</td><td>9<u>6</u></td><td>6</td><td>0.0002</td><td>1409</td></td> | 23 3 0.0003 273 8 0.0003 273 10 0.0004 273 11 0.0004 274 11 0.0009 275 10 0.0009 275 11 0.0009 275 11 0.0009 276 11 0.0009 277 8 0.0003 277 8 0.0003 277 8 0.0003 277 8 0.0003 278 10 0.0003 282 10 0.0003 282 10 0.0003 283 10 0.0003 284 10 0.0003 285 10 0.0003 286 8 0.0003 287 10 0.0003 288 0.0003 0.0003 290 0.0003 0.0003 20 0.0003 0.0003 20 0.0003 0.0003 20 0.0003 0.0003 <td>GDNOVMPK</td> <td>9<u>6</u></td> <td>6</td> <td>0.0002</td> <td>1409</td> | GDNOVMPK | 9 <u>6</u> | 6 | 0.0002 | 1409 |
| 278 8 0.0004 278 8 0.0004 202 9 0.0003 201 10 0.0003 202 1 0 0.0003 245 11 0 0.0003 250 10 0.0004 0.0004 250 10 0 0.0004 116 8 0.020 0.0004 116 9 0.0004 0.0004 116 9 0.0002 0.0002 250 10 0.0002 0.0002 270 8 0.0002 0.0002 271 8 0.0002 0.0002 272 8 0.0003 0.0003 273 8 0.0003 0.0003 284 10 0.0003 0.0003 278 8 0.0003 0.0003 28 0.0003 0.0003 0.0003 29 0.0003 0.0003 0.0003 20 0.0003 0.0003 20 0.0003 0.00 | 278 8 0.0004 278 8 0.0004 289 0.0003 246 10 0.0003 246 11 0.0003 247 11 0.0009 248 10 0.0009 250 8 0.0009 116 10 0.0009 116 10 0.0009 116 10 0.0009 117 8 0.0009 113 0.0009 0.0002 114 11 0.0009 113 0.0009 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 114 11 0.0009 1 | GLVGAÇA GLVGAOAPA | 3 5 | ∞ ⊆ | 0000 | 0141 |
| 278 1 278 1 280 1 281 10 282 1 284 10 285 10 286 10 287 1 288 0.0009 290 0.0009 290 0.0002 270 8 0.0003 271 8 0.0002 280 1 0.0002 290 1 0.0003 291 1 0.0003 292 0.0003 0.0003 293 0.0003 0.0003 294 1 0.0003 295 0.0003 0.0003 296 0.0003 0.0003 297 8 0.0003 298 0.0003 0.0003 299 0.0003 0.0003 200 0.0003 0.0003 200 0.0003 0.0003 200 0.0003 0.0003 200 0.0003 0.0003 </td <td>278 1 0.0003 282 1 0.0003 183 10 0.0003 245 11 0.0004 246 11 0.0009 247 11 0.0009 248 11 0.0009 250 10 0.0007 250 11 0.0002 250 11 0.0002 270 8 0.0002 271 8 0.0002 272 8 0.0002 273 11 0.0002 274 11 0.0002 275 10 0.0002 276 11 0.0002 277 8 0.0003 286 11 0.0009 290 0.0003 0.0003 201 10 0.0003 202 10 0.0003 203 10 0.0003 204 10 0.0003 205 10 0.0003 206 11 0.0003</td> <td>JETSVVK</td> <td>57 877</td> <td>2 %</td> <td>0.0003</td> <td>- t+ - t-</td> | 278 1 0.0003 282 1 0.0003 183 10 0.0003 245 11 0.0004 246 11 0.0009 247 11 0.0009 248 11 0.0009 250 10 0.0007 250 11 0.0002 250 11 0.0002 270 8 0.0002 271 8 0.0002 272 8 0.0002 273 11 0.0002 274 11 0.0002 275 10 0.0002 276 11 0.0002 277 8 0.0003 286 11 0.0009 290 0.0003 0.0003 201 10 0.0003 202 10 0.0003 203 10 0.0003 204 10 0.0003 205 10 0.0003 206 11 0.0003 | JETSVVK | 57 877 | 2 % | 0.0003 | - t+ - t- |
| 202 9 189 0 201 189 224 11 225 11 226 10 227 8 116 8 250 9 116 10 250 9 270 9 271 8 272 8 273 8 274 11 275 8 276 9 277 8 284 10 295 10 20003 10 20003 10 20003 10 20003 10 20003 10 20003 10 20003 10 20003 10 20009 10 20009 10 20009 10 20009 10 20009 10 20009 10 20009 10 | 202 9 189 0 201 189 224 10 225 10 226 10 227 10 228 11 239 0.0004 250 9 250 9 270 9 280 0.0002 290 0.0002 27 11 28 0.0002 29 0.0002 20 0.0002 21 0.0002 22 11 24 11 25 10 26 0.0003 27 10 28 0.0003 29 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 </td <td>IETSYVKVI H</td> <td>278</td> <td>•</td> <td>1000.0-</td> <td>1412</td> | IETSYVKVI H | 278 | • | 1000.0- | 1412 |
| 189 10 0.0003 201 10 0.0009 225 11 0.0009 245 10 -0.0009 25 11 -0.0004 45 11 -0.0004 25 11 0.0230 116 9 0.0430 116 10 0.0260 250 9 0.0002 27 11 0.0002 28 11 0.0002 29 0.0002 0.0003 31 9 0.0003 32 11 0.0003 33 8 0.0003 44 10 0.0003 248 11 0.0003 248 11 0.0003 248 11 0.0003 248 11 0.0003 248 11 0.0003 248 11 0.0003 248 11 0.0003 248 11 0.0003 248 11 0.0003 | 201 169 0.0093 202 245 11 0.0009 225 10 0.0009 45 11 0.0004 45 11 0.0004 116 8 0.0230 116 9 0.0430 116 11 0.0250 117 11 0.0002 250 9 0.0002 27 11 0.0002 27 11 0.0002 28 11 0.0002 29 0.0002 0.0002 20 11 0.0002 20 11 0.0002 20 11 0.0002 20 11 0.0002 20 11 0.0003 20 11 0.0003 20 11 0.0003 20 11 0.0003 20 11 0.0003 20 20 0.0003 20 20 0.0003 20 20 0.0003 | IIVLAIIA | 202 | = 0 | | 1414 |
| 201 120 8 -0.0009 245 11 -0.0004 225 10 -0.0004 45 11 -0.0004 45 11 -0.0004 116 8 0.0250 116 10 0.0260 230 9 0.0250 230 9 0.0002 237 8 1 247 9 0.0002 257 8 0.0003 266 11 0.0009 27 8 0.0003 28 10 0.0003 29 0.0003 0.0003 20 11 0.0009 20 10 0.0003 20 10 0.0003 20 10 0.0003 20 10 0.0003 20 10 0.0003 20 10 0.0003 20 10 0.0003 20 10 0.0003 20 0.0003 0.0003 | 201 120 245 245 246 110 252 247 248 248 248 248 248 248 248 248 248 248 | LGDNOVMPK | 681 | \ C | 0.0093 | 1415 |
| 245 11 -0.0009 246 11 -0.0004 45 10 -0.0004 45 11 0.020 116 8 0.020 116 9 0.0430 116 11 0.020 250 10 0.020 250 10 0.002 27 11 0.000 27 11 0.000 27 11 0.000 28 10 0.000 29 0.000 0.000 20 11 0.000 24 11 0.000 25 8 0.000 26 10 0.000 27 8 0.000 28 10 0.000 29 10 0.000 20 10 0.000 21 10 0.000 22 8 0.000 23 14 11 44 14 10 0.000 248 | 245 11 -0.0009 246 10 -0.0004 45 10 -0.0004 45 11 -0.0004 45 11 -0.0004 116 8 0.0250 116 9 0.0430 116 11 0.0260 250 10 0.0002 27 8 0.0002 28 11 0.0009 28 11 0.0009 262 11 0.0003 28 11 0.0003 28 11 0.0003 29 0.0003 0.0003 20 8 0.0003 20 10 0.0003 20 10 0.0003 20 11 0.0003 20 11 0.0003 20 11 0.0003 20 11 0.0003 20 11 0.0003 20 11 0.0003 20 11 0.0003 2 | LIIVLAIIA | 201 | 2 | | 1416 |
| 245 11 255 10 45 11 116 8 116 8 116 8 116 10 117 9 250 0 250 10 250 10 270 9 271 8 272 8 284 10 29 0 200 0 | 245 11 225 10 25 11 25 11 25 11 116 8 116 9 117 9 250 9 250 9 27 9 27 9 27 9 27 11 27 8 28 10 29 0.0002 20 0.0003 31 9 99 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0003 20 0.0 | LLKYRAR | 120 | . ∞ | -0.0009 | 1417 |
| 236 10 -0.0004 4 5 8 11 116 8 8 8 0.0250 116 9 9 0.0260 1250 9 0.0002 178 9 9 0.0002 178 9 9 0.0003 18 9 0.0003 19 9 9 9 0.0003 19 9 9 0.0003 19 9 9 10 0.0003 19 9 11 0.0003 19 9 11 0.0003 19 9 11 0.0003 19 9 11 0.0003 19 9 11 0.0003 19 9 11 0.0003 19 9 11 0.0003 | 236 45 45 45 45 45 45 45 45 46 416 48 88 40029 40020 4 | LMQDLVQENY | 245 | = | | 1418 |
| 255 110 -0.0004 256 11 -0.0004 116 9 0.0430 116 10 0.0260 250 9 0.0260 250 9 0.0027 250 9 0.0002 27 8 0.0002 28 0.0002 27 8 0.0003 28 0.0003 29 0.0003 20 8 0.0003 20 8 0.0003 20 10 0.0003 22 8 0.0003 23 10 0.0003 24 10 0.0003 24 11 0.0003 24 11 0.0003 24 11 0.0003 24 11 0.0003 25 10 0.0003 26 11 0.0003 27 14 10 0.0003 28 11 0.0003 29 11 0.0003 | 255 110 -0.0004 256 8 8 0.02390 116 9 9 0.02390 117 10 0.0220 250 9 9 0.00027 257 111 0.0002 258 11 0.0002 259 11 0.0003 250 11 0.0003 250 10 0.0003 250 10 0.0003 251 8 8 0.0003 252 8 8 0.0003 253 8 8 0.0003 254 8 8 0.0003 255 8 8 0.0003 257 11 0.0003 258 8 0.0003 259 10 0.0003 250 10 0.0003 250 10 0.0003 251 8 8 0.0003 252 8 8 0.0003 253 8 8 0.0003 254 8 8 0.0003 255 8 8 0.0003 267 11 0.0003 27 14 14 16 8 8 11 | MQDLVQENY | 246 | 10 | | 1419 |
| 45 11 116 8 0.0290 116 8 0.0290 116 10 0.0260 116 10 0.0260 250 10 0.0027 250 10 0.0027 270 11 0.0002 271 8 0.0002 272 8 0.0003 284 11 0.0003 295 10 0.0003 296 10 0.0003 297 10 0.0003 298 10 0.0003 299 10 0.0003 200 10 0.0003 201 10 0.0003 202 8 0.0003 203 10 0.0003 204 11 0.0003 206 11 0.0003 207 0.0003 0.0003 208 11 0.0003 209 0.0003 0.0003 200 0.0003 0.0003 200 | 25 45 116 8 0.0290 116 9 0.0430 116 10 0.0260 117 9 0.0027 250 9 0.0002 250 10 0.0002 27 8 10 0.0002 27 8 11 0.0002 26 11 0.0003 0.0003 27 8 8 0.0003 28 10 0.0003 0.0003 27 8 8 0.0003 28 10 0.0003 0.0003 29 10 0.0003 0.0003 20 8 10 0.0003 20 10 0.0003 0.0003 21 10 0.0003 0.0003 22 10 0.0003 0.0003 24 10 0.0003 0.0003 248 11 0.0002 248 11 0.0002 260 11 0.0003 27 | SMLEVFEGR | 225 | 10 | -0.0004 | 1420 |
| 15 | 116 8 0,0290 116 9 0,0430 116 11 0,0260 1250 10 0,0260 250 9 0,0002 97 11 0,0002 97 11 0,0002 113 11 0,0002 227 8 10 0,0002 246 11 0,0003 0,0003 25 10 0,0003 0,0003 26 8 0,0003 0,0003 27 10 0,0003 0,0003 28 10 0,0003 0,0003 28 10 0,0003 0,0003 29 11 0,0003 0,0003 20 10 0,0003 0,0003 20 10 0,0003 0,0003 20 10 0,0003 0,0003 20 10 0,0003 0,0003 20 10 0,0003 0,0003 20 10 0,0003 0,0003 20 | VEVTLGEVPA | 45 | = | | 1421 |
| 116 8 0.0250 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.17 1. | 116 8 0.0230 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.16 1.17 1. | VGAQAPA | 25 | ∞ | | 1422 |
| 116 9 0.0430 116 11 11 11 11 11 1250 10 10 0.0260 178 9 9 0.0002 178 9 9 0.0002 178 9 9 0.0002 142 11 11 11 0.0002 142 11 11 0.0003 154 16 17 0.0003 155 16 17 0.0003 156 17 18 0.0003 157 158 0.0003 158 0.0003 158 0.0003 159 160 0.0160 150 17 18 151 151 151 152 153 154 154 154 155 155 155 155 155 155 | 116 10 0.02430 116 117 1250 0.02640 117 11 | VHFLLLK | 911 | ~ | 0.0290 | 1423 |
| 16 | 116 | VHFLLLKY | 911 | 6 | 0.0430 | 1424 |
| 116 | 250 9 11 250 10 250 10 250 10 250 10 27 8 11 27 8 8 0.0002 254 10 256 11 262 262 8 8 262 262 8 8 263 10 27 8 8 0.0003 264 11 27 8 8 0.0003 27 8 8 0.0003 28 8 0.0003 29 10 8 8 0.0003 20 2 8 8 8 0.0003 20 3 30 3 8 8 0.0003 20 4 8 8 8 0.0003 20 5 8 8 6.0003 20 6 8 8 6.0003 20 7 8 8 8 7.0003 20 8 8 8 7.0003 20 8 8 8 7.0003 20 8 8 8 7.0003 20 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | VHFLLKYR | 116 | 10 | 0.0260 | 1425 |
| 250 250 250 178 178 9 9 9 9 97 18 11 142 142 160 9 9 9 9 9 9 170 170 170 170 170 170 170 170 170 170 | 250 250 250 178 97 97 97 97 97 98 111 99 110 99 99 99 99 99 99 99 10 99 99 10 99 10 90 00003 22 2 2 2 31 44 144 144 144 144 248 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | VHFLLLKYRA | 911 | = | | 1426 |
| 178 9 9 0.0027 97 9 9 0.0002 227 8 8 -0.0009 113 111 111 114 119 0.0003 265 110 0.0003 265 110 0.0003 265 8 8 0.0003 265 10 8 8 0.0003 267 11 0.0003 268 8 10 0.0003 269 10 0.0003 27 18 8 0.00003 28 10 0.0003 29 11 148 8 8 114 248 8 8 11 | 250 178 9 0.0002 97 9 0.0002 27 8 -0.0009 113 11 0.0002 142 10 0.0002 26 11 0.0003 26 11 0.0003 26 8 0.0003 26 8 0.0003 27 10 0.0003 28 10 0.0003 29 10 0.0003 44 10 0.0160 248 8 0.0002 248 8 0.0002 248 8 11 248 8 0.0002 | VQENYLEY | 250 | 6 | | 1427 |
| 178 9 97 9 97 9 97 9 113 11 142 10 143 11 264 11 31 9 99 9 99 10 262 8 263 8 264 10 10 0.0003 27 8 10 0.0003 10 0.0003 148 10 144 8 144 11 144 11 144 11 248 8 248 11 | 97 9 97 9 97 9 113 11 142 10 142 10 266 11 31 9 99 10 99 0.0003 262 8 263 8 27 10 10 0.0003 2 8 2 8 2 8 148 11 144 8 144 10 248 11 248 11 248 8 248 11 248 11 250 10 144 10 250 10 248 11 | VQENYLEYR | 250 | 10 | 0.0027 | 1428 |
| 227 11 | 97 227 11 113 11 142 11 143 10 264 10 31 9 265 11 99 0.0003 99 10 262 8 263 8 264 10 27 10 28 0.0003 303 8 14 10 144 11 144 10 248 8 248 8 250 11 144 10 250 11 248 8 248 8 250 11 260 8 | VICEULST FDVI FCFF | 1/8 | ~ | 6000 | 1429 |
| 227 113 1142 115 116 0.0200 117 256 119 266 111 0.0002 267 268 111 0.0003 269 260 10 0.0003 27 28 28 28 29 20003 2 | 227 113 113 1142 115 116 0.00002 54 110 0.0002 266 11 11 9 9 99 99 99 10 0.0003 262 2 2 2 2 2 303 8 8 0.0003 303 8 8 0.00003 303 8 8 11 14 14 11 11 11 12 12 13 13 13 14 14 11 12 14 12 18 11 11 12 13 13 13 14 14 18 18 18 18 18 18 18 18 18 18 18 18 18 | FPDI ESEFOA | 6 | | 2000.0 | 1430 |
| 113 111 0.0200 142 266 111 0.0002 31 99 9 9 0.0003 32 62 8 8 0.0003 262 8 8 0.0003 262 8 8 0.0003 303 8 8 0.0003 59 10 0.0003 44 14 11 18 10 0.0002 | 113 | I EVEEGR | 1,00 | _ ~ | 9000 0- | 1641 |
| 142 10 00002 24 10 -0.0009 31 99 99 9 0 0.0003 262 8 8 0.0003 262 8 8 0.0003 303 8 8 0.0003 148 10 0.0160 27 11 8 8 0.0002 28 29 10 0.0003 29 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 142 10 54 10 266 11 99 9 99 9 99 10 262 8 263 8 27 8 303 8 10 0.0003 29 10 144 10 144 11 248 8 248 8 248 8 250 11 260 8 | VELVHELLIK | 113 | o = | 0.020 | 1433 |
| 24 10 -0.0009 31 9 9 0.0003 99 99 99 10 0.0003 262 8 8 0.0003 27 10 8 0.0003 303 8 8 0.0003 59 10 0.0003 29 11 8 8 0.0002 248 11 11 | 54 10 266 11 266 11 31 9 99 9 99 10 262 8 27 8 28 0.0003 303 8 10 0.0003 29 11 144 10 144 11 248 8 248 8 250 11 248 8 250 11 260 8 | CODFFPVIF | 142 | | 0.0002 | 1434 |
| 266 11 9 -0.0009 31 9 9 0.0003 99 99 99 90 0.0003 262 8 8 0.0003 27 10 0.0003 303 8 8 -0.0009 59 10 0.0003 148 10 0.0160 29 11 1 144 11 | 266 117 -0.0009 31 9 9 0.0003 99 99 10 0.0003 262 8 8 0.0003 27 10 8 8 0.0003 303 8 8 -0.0009 59 11 0 0.0160 29 11 8 8 0.0002 24 8 8 8 0.0002 25 11 8 8 0.0002 260 8 8 | AADSPSPPH | 54 | | | 1435 |
| 31 9 9 0,0003 99 9 0,0003 262 8 8 0,0003 2 10 0,0003 303 8 8 -0,0009 59 10 0,0003 10 0,0003 11 8 11 144 8 8 0,0002 | 31 9 9 0,0003 99 9 10 0,0003 262 8 8 0,0003 2 2 8 8 0,0003 333 8 8 -0,0009 59 10 0,0003 148 10 0,0160 29 11 8 8 0,0002 248 8 8 0,0002 | ACYEFLWGPR | 266 | 2 = | 6000.0- | 1436 |
| 99 9 9 0.0003 262 8 8 0.0003 2 2 10 8 8 0.0003 2 2 8 8 0.0003 303 8 8 0.0009 59 10 0.0003 148 10 0.0160 29 11 8 8 8 248 8 8 | 99 9 9 0.0003 262 8 8 0.0003 2 2 10 8 8 0.0003 303 8 8 -0.0009 59 10 0.0003 2 10 0.0003 2 10 0.0003 2 11 8 8 0.0000 2 14 8 8 0.0002 2 14 11 8 8 8 0.0002 2 2 8 8 0.0002 2 14 8 8 0.0002 2 2 8 8 0.0002 2 2 8 8 0.0002 | A TEEQQTA | 31 | . 6 | | 1437 |
| 99 10 0.0003 262 8 8 0.0003 2 2 10 8 0.0003 303 8 8 0.0009 59 10 0.0003 44 11 11 0.0002 | 99 10 0.0003 262 8 8 0.0003 2 2 8 8 0.0003 3 3 8 8 0.0003 3 3 9 10 0.0003 5 9 10 0.0003 2 9 11 0.0160 2 9 11 8 8 8 0.0002 2 144 8 8 8 11 244 2 48 8 8 11 2560 | OLESEFOA | 66 | . 6 | 0.0003 | 1438 |
| 262 8 262 10 2 2 8 303 8 0,0003 303 8 8 -0,0009 59 10 0,0160 29 11 8 8 0,0002 144 11 11 | 262 8 8 0.0003 2 8 8 0.0003 2 10 8 0.0003 303 8 8 -0.0009 59 10 0.0160 29 11 8 8 8 8 248 8 8 250 248 8 8 8 11 | JLESEFQAA | 66 | 01 | 0.0003 | 1439 |
| 262 10 0.0003 2 8 0.0003 303 8 0.0003 59 10 0.0160 29 11 0.0160 144 11 11 11 11 11 11 11 11 11 11 11 11 | 262 10 0.0003 2 8 0.0003 303 8 0.0003 59 10 0.0160 29 11 0.0160 144 8 8 0.0002 248 8 8 8 248 8 8 250 8 8 | SSDPACY | 262 | 8 | | 1440 |
| 2 8 0.0003 303 8 6.00003 59 10 0.0160 29 11 0.0160 144 8 8 0.0002 248 11 | 2 8 0,0003 303 8 8 -0,0009 59 10 0,0160 29 11 8 0,0160 144 11 0,0002 248 8 8 111 | GSDPACYEF | 262 | 10 | | 1441 |
| 2 10 0,0003 393 8 -0,0009 59 10 0,0160 29 11 8 0,0002 144 11 11 11 | 2 10 0,0003 333 8 -0,0009 59 10 0,0160 29 11 0 0,0160 144 10 8 0,0002 144 11 8 0,0002 248 8 8 11 | JEQRSQH | 2 | 8 | | 1442 |
| 303 8 -0.0009 59 10 0.0160 148 10 0.0160 29 11 8 8 144 104 11 248 8 | 303 8 -0.0009 59 10 0.0160 148 10 0.0160 29 11 8 8 144 10 10 0.0002 248 8 8 250 8 | EQRSQHCK | 2 | 10 | 0.0003 | 1443 |
| 59 10 0.0160 148 10 0.0160 29 11 144 8 144 10 0.0002 248 8 | 59 10 148 10 29 11 144 8 144 11 248 8 248 8 250 8 | HERALR | 303 | - ∞ | -0.0009 | 1444 |
| 148 10 0.0160 29 11 0.0160 144 11 0.0002 248 8 8 248 11 | 148 10 0.0160 29 11 0.0160 144 8 0.0002 144 11 11 248 8 8 250 8 | SPPHSPQGA | 59 | 10 | | 1445 |
| 29 11 144 8 144 10 248 8 8 248 11 | 29 11 144 8 144 10 248 8 260 8 | /IFSKASEY | 148 | 10 | 0.0160 | 1446 |
| 144 8 0.0002 144 11 248 8 8 | 144 8 0.0002 144 11 0.0002 248 8 11 260 8 | APATEEQQTA | 29 | = | | 1447 |
| 144 \$10 0.0002 144 \$11 \$14 248 \$8 248 \$1 | 144 10 0.0002 144 11 14 248 8 248 11 260 8 | DFFPVIF | 144 | ∞ | | 1448 |
| 144 11 248 8 248 11 | 144 11 248 8 248 11 260 8 | DFFPVIFSK | 144 | 01 | 0.0002 | 1449 |
| 248 8 248 11 | 248 8 248 11 260 8 | DFFPVIFSKA | 144 | = | | 1450 |
| 248 11 | 248 11 260 8 | DLVQENY | 248 | 8 | | 1451 |
| | 260 8 | DLVQENYLEY | 248 | = | | 1452 |

| | Mag | Table XVI B Mage 3 A03 Motif Pentides with Rinding Deta | | |
|--------------------------|--------------------|---|---------|------------|
| | | 2 AUS MOUIL LEDUNCS WITH DINNING DATA | | ; |
| Sequence | Position | No. of Amino Acids | A*0301 | SEQ ID NO. |
| AALSRKVA | 101 | 8 | | 1491 |
| ACYEFLWGPR | 267 | 0 : | 0.0032 | 1492 |
| ACTER WOLKS | 707 | <u> </u> | 90000 | 1494 |
| Allaredoca | 207 | √ 2 | | 1495 |
| ALGLVGAQA | 22 | . 6 | 0.0003 | 1496 |
| ALGLVGAQAPA | 23 | = : | | 1497 |
| ALSKKVAELVH | 801 | = (| | 1498 |
| ALVEISYVK ASSI PTTMNV | //7 | ο <u>-</u> | 0.0270 | 1500 |
| ASSSI OLVF | 154 | ⊇ σ | 0.001 | 120 |
| ATCLGLSY | 179 | ∕ ∞ | | 1502 |
| ATEEQEAA | 32 | 8 | | 1503 |
| DLESEFQA | 00: | ∞ (| | 1504 |
| DLESELQAA DSII GDBV | 100 | ~ • | V000 0- | 5051 |
| DSILCULA DOIL GDBKK | 236 | æ c | -0.0004 | 1507 |
| EALGI VGA | 23 | ~ ∝ | 6000.0- | 1508 |
| EALGLVGAQA | 21 | 01 | 0.0003 | 1509 |
| EDSILGDPK | 235 | 6 | 0.0003 | 1510 |
| EDSILGDPKK | 235 | 01 | 0.0003 | 1511 |
| EFLWGPRA | 270 | ∞ (| | 1512 |
| EFÇAALSK EEGAALSBV | 2 2 | ∞ ດ | 0000 | 5151 |
| EFOAL SRKVA | 100 | ^ = | 2000.0 | 1515 |
| EGDCAPEEK | 212 | 6 | 0.0002 | 1516 |
| EGLEARGEA | 4 | . 6 | 0.0003 | 1517 |
| ELMEVDPIGH | 165 | 10 | 0.0003 | 1518 |
| ELSVLEVF | 224 | ∞ : | . 0000 | 6151 |
| ELSVEVFECK | 577 118 | = < | -0.0009 | 0751 |
| ELVAFLEEN ELVHELLIKV | 511 | 6 | 0.0045 | 1522 |
| ELVHFLLLKYR | 115 | 2 = | 0.0011 | 1523 |
| ESEFQAALSR | 102 | : 01 | 0.0002 | 1524 |
| ESEFQAALSRK | 102 | . = | 0.0002 | 1525 |
| ETSYVKVLH | 280 | 6 | | 1526 |
| EISYVKVLHH EVDPIGHI V | 780 1 68 | 01 | 0 000 0 | 1528 |
| EVDFIGHE! | 897 | 7 | 0.0002 | 6251 |
| EVTLGEVPA | 47 | - 6 | 0.0003 | 1530 |
| EVTLGEVPAA | 47 | 10 | 0.0003 | 1531 |
| FATCLGLSY | 178 | o • | 0.0003 | 1532 |
| FFFVIFSA | 146 | • • | 0 0003 | 1534 |
| FLLLKYRA | 611 | \ ∞ | | 1535 |
| FLLLKYRAR | 611 | 6 | | 1536 |

| | | Table XVI B Mage 3, A03, Motif Peptides with Binding Data | | |
|-----------------------------|------------|---|--------|--------------|
| Sequence | Position | No. of Amino Acids | A*0301 | SEQ ID NO. |
| FVQENYLEY | 250 | 6 | | 1537 |
| FVÇENYLEYK GASSLPTTMNY | 50 67 | 10 | 0.0009 | 1538 |
| GDCAPEEK | 213 | ∞ • | | 1540 |
| GDNOIMPKA | 161 | · • | 0.0003 | 1542 |
| GDPKKLLTQH | 240 | 10 | 0.0003 | 1543 |
| GDPKKLLTQHF | 240 | =: | | 1544 |
| GLEARGEA | | ∝ | | 1545 |
| GLLGDNQIMPK | 188 | · = | 0.1300 | 1547 |
| GLIIVLA | 500 | ∞: | | 1548 |
| GLII VLAIIA GLVGAOAPA | 24 24 | _ 0 | 0 0003 | 1550 |
| GSDPACYEF | 263 | , 6 | | 1551 |
| GSVVGNWQY | 137 | 6 | | 1552 |
| GSVVGNWQYF | 137 | 01 | 0.0020 | 1553 |
| GSV VGNWQ1 rr HCKPEEGLEA | /s1 6 | <u> </u> | 0 0003 | 1554 |
| HCKPEEGLEAR | . 6 | 2 = | | 1556 |
| HFLLLKYR | 118 | ∵ 80 | | 1557 |
| HFLLLKYRA | 8 - | 6 | 0.0016 | 1558 |
| HEVOENYLEY | 249 | <u> </u> | 0.0014 | 1560 |
| HFVQENYLEYR | 249 | 2 = | | 1561 |
| НІЅҰРРСН | 298 | 8 | | 1562 |
| HMVKISGGPH | 289 | 01 | | 1563 |
| IFATCLGLSY | 177 | s O | 0.0005 | 1565 |
| IGHLYIFA | 172 | :∞ | | 1566 |
| IIAREGDCA | 208 | 0.6 | | 1567 |
| IIVLAIIAR | 203 | ~ • | 6900.0 | 1569 |
| ISGGPHISY | 293 | . 6 | 0.0003 | 1570 |
| IVLAIIAR | 204 | ∞ : | 0.0053 | 1571 |
| KASSSI OI VE | 8,51 | D 9 | 0 0003 | 15/2 |
| KISGGPHISY | 292 | . 01 | | 1574 |
| KVAELVHF | 112 | 82 | 1 | 1575 |
| KVLHHMVK LAIIAREGDCA | 285 206 | ∞ = | 0.0580 | 1576 |
| LGDNQIMPK | 190 | ; 00 | | 1578 |
| LGDNQIMPKA LGDPKKLLTQH | 190 239 | 10 | 0.0003 | 1579 1580 |
| LGLVGAQA I GI VGAQAPA | £ £ | ∞ <u>-</u> | 0 0003 | 1581 |
| | ì | 2 | 000000 | - |

| | | Table XVI B Mage 3 A03 Motif Peptides with Binding Data | | |
|---------------------------|------------|---|---------|------------|
| Sequence | Position | No. of Amino Acids | A*0301 | SEQ ID NO. |
| TGSVVGNWQY | 136 | 01 | 0.0003 | 1583 |
| LGSVVGNWQYF | 136 | := | | 1584 |
| LIIVLAIIA | 202 | 6 | | 1585 |
| LIIVLAIIAR | 202 | 10 | 0.0280 | 1586 |
| LLGDNQIMPK | 189 | 10 | 0.0200 | 1587 |
| LLGDNQIMPKA | 189 | = | | 1588 |
| LLIIVLAIIA | 701 | 01 | | 1589 |
| LLIIVLAIIAK | 107 | Ξ, | 0.0021 | 1590 |
| I TOHEVOENV | 245 | ∞ : | 6000.0- | 1661 |
| LMEVDPIGH | 991 | - 0 | 0.0002 | 1593 |
| LMEVDPIGHLY | 991 | . = | | 1594 |
| LSRKVAELVH | 109 | .01 | 0.0002 | 1595 |
| LSRKVAELVHF | 109 | = | | 1596 |
| LSVLEVFEGR | 225 | 01 | -0.0006 | 1597 |
| LTQHFVQENY | 246 | 10 | 0.0003 | 1598 |
| LVETSYVK | 278 | ∞ ' | -0.0004 | 1599 |
| LVETSYVKVLH | 278 | | | 1600 |
| LVEVTLGEVPA | \$ 5 | = ' | | 1091 |
| LVGAÇAFA | 9 | ∞ (| | 1602 |
| LVHFLLLK | 9 7 | ∞ (| 0.0290 | 1603 |
| LVHFLLLKYR | 9 9 9 | λ <u>C</u> | 0.0450 | 509 |
| LVHFLLLKYRA | 911 | 2 == | | 9091 |
| MLGSVVGNWQY | 135 | : = | | 1607 |
| MVKISGGPH | 290 | . 6 | 0.0003 | 1608 |
| PACYEFLWGPR | 266 | = | -0.0009 | 6091 |
| PATEEQEA | ₩ ; | ∞ . | | 1610 |
| PAIEEQEAA | <u>.</u> 6 | 6 | 0.0003 | 1191 |
| PDI ESEFÇA | £ 8 | ον 2 | 0.0003 | 7191 |
| PDPOSPOGA | 8 8 | 29 | 0.0003 | 5191 |
| PGSDPACY | 262 | 2 ∝ | | 1615 |
| PGSDPACYEF | 262 | 01 | | 1616 |
| PIGHLYIF | 171 | . 8 | | 1617 |
| PIGHLYIFA | 171 | 6 | | 8191 |
| PLEQRSQH | 7 | ∞ ` | | 1619 |
| PLEQRSQHCK | 2 | 01 | 0.0003 | 1620 |
| PLHEWVLK PETERNI ESSE | 503 | ∞ ; | -0.0009 | 1621 |
| rairruceaer Oaai sekva | 5 YO | _ 0 | | 7791 |
| OAPATEEOEA | <u> </u> | 10 | 0.0003 | 1624 |
| <u> </u> | 29 | : - | | 1625 |
| QVPGSDPA | 260 | 8 | | 1626 |
| QVPGSDPACY | 260 | 0. | | 1627 |
| KALVEISI | 0/7 | × | | 9701 |

| •. | Mage | <u>Table XVI B</u> Mage 3 A03 Motif Pentides with Binding Data | | |
|-------------------------|------------|---|---------|------------|
| Sequence | Position | No. of | A*0301 | SEQ ID NO. |
| | | Amino Acids | | |
| RALVETSYVK | 276 | 10 | 06100 | 1629 |
| RAREPVTK | 125 | 8 | -0.0009 | 1630 |
| RAREPVTKA | 125 | 6 | | 1631 |
| RGEALGLVGA | 61 | 10 | 0.0003 | 1632 |
| SDPACYEF | 264 | 8 | | 1633 |
| SGGPHISY | 294 | ∞ | | 1634 |
| SILGDPKK | 237 | 8 | -0.0009 | 1635 |
| SLPTTMNY | 70 | 80 | | 1636 |
| SSLPTTMNY | 69 | 6 | | 1637 |
| SSSLQLVF | 155 | 8 | | 1638 |
| STFPDLESEF | % | 10 | 0.0002 | 1639 |
| SVLEVFEGR | 226 | 6 | 0.0003 | 1640 |
| SVVGNWQY | 138 | ∞ | | <u>₹</u> |
| SVVGNWQYF | 138 | 6 | 0.0002 | 1642 |
| SVVGNWQYFF | 138 | 01 | 0.0085 | 1643 |
| TFPDLESEF | 97 | 6 | 0.0002 | 1644 |
| TFPDLESEFQA | 97 | | | 1645 |
| TLGEVPAA | 49 | 8 | | 1646 |
| TMNYPLWSQSY | 74 | = | | 1647 |
| TSYVKVLH | 281 | 88 | | 1648 |
| TSYVKVLHH | 281 | 6 | 0.5900 | 1649 |
| VAELVHFLLLK | 113 | = | -0.0002 | 1650 |
| VDPIGHLY | 169 | 8 | | 1651 |
| VDPIGHLYIF | 691 | 10 | 0.0003 | 1652 |
| VDPIGHLYIFA | 169 | = | | 1653 |
| VGNWQYFF | 140 | ∞ | | 1654 |
| VLEVFEGK | 227 | ∞ | 9100.0 | 1655 |
| VTLGEVPA | 48 | 8 | | 1656 |
| VTLGEVPAA | 48 | 6 | 0.0003 | 1657 |
| VVGNWQYF | 139 | ∞ | | 1658 |
| VVGNWQYFF | 139 | 6 | 0.0022 | 1659 |
| WGPKALVEISY | 2/3 | = ' | | 1990 |
| YFFFVIFSK VFFPVIFSKA | 145 145 | ∞ | 0.0020 | 1661 |
| YIEATCI GLSY | 176 | 2 = | 0000 | 7001 |
| YVKVLHHMVK | 283 | 01 | 0.0020 | 1664 |
| | | | | |

| Position 55 56 75 76 76 76 76 76 76 76 76 76 76 76 76 76 | Table XVII A Mage 2 A11 Motif Peptides with Binding Data | No. of A*1101 SEQ ID NO. Amino Acids | | 10 0.0035 1666 | <u> </u> | . 11 0.0007 1668 | _ | _ | _ | 9 0.0022 1672 | | 0.0005 | 0.0025 | | | | 0.0002 | 1891 1000:0 6 | 0.0008 | 0.0010 | 0.0003 | 1500.0 | | 6891 | | | 0,0002 | | | | 0401 0401 1 | | 6691 | | 0.0047 | | | 0.0002 | | 0,0018 1707 | | | | 6021 |
|--|--|--------------------------------------|----|----------------|----------|------------------|---|-----|----|---------------|-----|--------|--------|-----|-----|-----|------------|---------------|--------|-----------|--------|--------|------|------|-----|-----|--------|-----|-----|-------|-------------------|-----|------|-----|--------|--|-----|--------|-----|-------------|-----|-----|-----|------|
| Sequence AADSPSPPH ACYEFLWGPR ADSPSPPH ACYEFLWGPR ASPSPPH ALIETSYVK ASSESTTINY DLVQENYLEY DLVQENYLEY DLVQENYLEY DLVQENYLEY DLVQENYLEY BSSYFAHPR EDSVFAHPR EDSVFAHPR EDSVFAHPR EDSVFAHPR EDSVFAHPR EDSVFAHPR ELSMLEVFEGR ELVHFLLLK ENVEVNISH ETSYVKVLH HFLLKYRAR GDCAPEEK GDCAPEEK GDCAPEEK GDCAPEEK HFLLKYRAR HFLLKYRAR HISYPPLH HISYPPLH HISYPPLH HISYPPLH HISYPPLH HISYPPLH HISYPPLH HISYPPLH HISYPPLH HISYPPLH | Mage 2 A11 | | 55 | 267 | 26 | | | 772 | 89 | 145 | 249 | 236 | 236 | 235 | 235 | 101 | 201 | 212 | | <u>S1</u> | SII : | 52. | +C-1 | 102 | 280 | 280 | 165 | 891 | 146 | δ | - 53 | 213 | 161 | 294 | | | 118 | 118 | 298 | 298 | 783 | 03- | 150 | 150 |

| | Table XVII A | | |
|------------|--|--------|-----|
| Mage 2 All | 2 All Motif Peptides with Binding Data | | |
| Position | No. of | A*1101 | SEC |
| A | Amino Acids | | |

| Decision No. of Animo Acids Animo Acid | - | | Jable XVII A Mage 2 AII Motif Peptides with Binding Data | Iding Data | |
|--|--------------------------|------------|--|------------|------------|
| 177 177 10 0,0002 10 0,0002 10 10 10 10 10 10 10 | Sequence | Position | No. of Amino Acids | A*1101 | SEQ ID NO. |
| 109 109 109 109 100 100 100 100 100 100 | ILVTCLGLSY | 177 | 01 | 0.0002 | 1171 |
| 112 | ISKKMVELVH ISVDDI UED | 60. | 0.0 | 0.0002 | 1712 |
| 252 253 254 255 257 257 257 257 257 257 257 257 257 | KAEMI FSVI R | 133 | Σ - | 0.0280 | 1/13 |
| 255 278 278 278 278 278 278 278 278 278 278 | KIGGEPHISY | 292 | 2 2 | 6,000 | 1714 |
| 190 4 | KVLHHTLK | 285 | 2 ∞ | 0.0100 | 1716 |
| 7. | LGDNQVMPK | 061 | , 6 | 1900'0 | 1717 |
| 7. 189 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | LIETSYVK | 278 | . 00 | 0.0027 | 1718 |
| 189 | LIETSYVKVLH | 278 | = | | 1719 |
| 170 8 00004 172 245 11 1 00004 246 10 10 0 00001 116 8 8 0 01500 117 10 0 01002 250 10 10 0 00002 178 256 11 1 0 01002 2 2 8 8 0 00002 2 3 8 8 0 00003 148 144 10 10 00003 177 256 11 1 0 00003 178 256 11 1 0 00003 179 250 10 10 00003 170 250 10 10 00003 171 11 11 11 11 11 11 11 11 11 11 11 11 | LIGDNQVMPK | 681 | 01 | 0.0014 | 1720 |
| F. 245 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | CLLKYRAR | 120 | ∞ | -0.0004 | 1721 |
| 246 10 0.00001 1.5 | LIMQDLVQENY | 245 | | | 1722 |
| 1.55 1.0 0.10001 1.16 8 8 0.11500 1.16 10 10 0.10022 1.25 10 10 0.10022 1.25 250 10 0.10022 1.25 254 10 0.1002 2 | CMQDLVQENY | 246 335 | 01 | | 1723 |
| 110 | VIETTIV | 577 | 2, | 0.000 | 1/24 |
| 150 10 10 10 10 10 10 10 | VHFLLLKY | 91.7 | ∞ c | 0.100 | 1725 |
| 250 250 178 178 178 178 178 178 178 178 178 178 | VHFILLKYR | 91 | 6 | 0.0100 | 1727 |
| 15 | LVOENYLEY | 250 | 2 თ | 77000 | 1278 |
| 178 178 9 9 178 18 178 18 18 19 19 19 19 19 1 | LVOENYLEYR | 250 | \ <u>C</u> | 68000 | 1729 |
| K 113 | UNTCLGLSY | 178 | 6 | | 1730 |
| K 113 11 0.0120 366 11 0.0002 2 11 0.0002 303 8 0.0002 148 10 0.0003 148 8 0.0033 149 10 0.0033 144 10 0.0033 15 10 0.0033 16 0.0033 17 8 0.0003 125 8 0.0003 126 9 0.0001 69 9 0.0001 69 9 0.0001 74 8 0.0550 129 9 0.0550 129 9 0.0550 129 9 0.0550 129 9 0.0550 | MLEVFEGR | 227 | . 00 | -0.0004 | 1731 |
| 266 11 | MVELVHFLLLK | 113 | = | 0.0120 | 1732 |
| 7R 266 11 -0,0002 2 8 0,0002 303 8 0,0004 148 10 0,0003 144 10 0,0003 248 8 0,0003 77 8 0,0750 276 8 0,0003 125 8 0,0003 8 0,0003 69 9 0,0001 88 9 0,0001 87 10 0,0001 72 10 0,0010 237 8 0,0001 248 8 0,0050 290 9 0,0050 291 9 0,0050 291 9 0,0050 291 9 0,0050 291 9 0,0050 291 9 0,0050 291 9 0,0050 291 9 0,0050 291 9 0,0050 291 9 0,0050 292 9 0,0050 293 9 0,0050 294 9 0,0050 295 0,0050 0,0050 200 <td< td=""><td>AADSPSPPH</td><td>54</td><td>01</td><td></td><td>1733</td></td<> | AADSPSPPH | 54 | 01 | | 1733 |
| 262 8 8 0.0002 2 10 0.0002 2 2 10 8 0.0002 303 8 8 0.0003 144 10 0.0033 248 8 8 8 0.0003 276 10 8 8 0.0003 70 8 8 0.0003 71 10 0.0001 69 9 0.0001 72 10 10 0.0001 73 72 10 10 0.0010 74 8 8 0.00550 | PACYEFLWGPR | 266 | = | -0.0002 | 1734 |
| 2 10 0.0002 303 8 8 0.0004 148 10 0.0033 144 10 0.0033 144 10 0.0033 145 11 0.0003 15 248 11 10 0.0033 17 266 8 8 0.0050 17 20 8 8 0.0001 18 8 0.0001 18 8 0.0001 18 8 0.0001 18 8 0.0001 18 8 0.0001 18 8 0.0001 18 8 0.0001 18 8 0.0001 19 0.0002 19 0.0002 19 0.0002 19 0.0002 19 0.0003 | GSDPACY | 262 | ∞ · | | 1735 |
| 303 8 8 | PLEQRSQH | 7 (| ∞ ; | • | 1736 |
| H 148 10004 K 148 10 0.0003 K 248 8 8 0.0003 CY 256 8 8 0.00750 K 276 125 8 8 0.0002 R 226 9 0.0001 R 8 7 10 0.0002 R 8 7 10 0.0001 R 8 8 9 0.00001 R 97 10 0.0010 R 1237 8 8 0.00810 C 10 0.0550 | CLECKSCHCK | 7 | 0 | 0.0002 | 1737 |
| K 144 10 0,0033 K 248 8 8 8 0,0083 LEY 248 11 SY 256 10 10 0,0033 K 276 10 R 226 9 0,0001 R 8 9 0,0001 R 8 9 0,0001 R 8 9 0,0001 R 8 7 10 0,0002 R 8 9 0,0001 R 8 9 0,0001 R 8 9 0,0001 R 8 9 0,0001 R 9 9 0,0001 | PLHEKALK | 303 | ∞ : | -0.0004 | 1738 |
| LEY 248 8 8 0.0083 LEY 248 8 11 27 256 8 8 0.0750 R 226 9 0.0001 R 226 9 0.0001 R 87 10 0.0002 R 72 10 0.0002 R 87 10 0.0002 R 72 10 0.0001 R 72 10 0.0002 R 8 9 0.0002 R 8 9 0.0001 R 97 10 0.0010 R 125 8 8 0.0550 | VIFSNASET | 84- | <u>0</u> : | 0.0033 | 1739 |
| LEY 248 8 8 0.0750 K 276 8 8 0.0750 K 276 8 8 0.0003 N 88 9 9 0.0001 R 87 10 0.0002 R 87 10 0.0002 R 87 10 0.0001 R 97 10 0.0910 N 14 8 8 0.0550 | JUFFFVIFSK Sprivorsky | 44. | 01 | 0.0083 | 1740 |
| LEY 248 III 250 248 III 8 8 0.0750 70 8 8 -0.0003 71 8 8 0.0001 8 8 0.0001 8 8 0.0001 8 8 0.0001 8 8 0.0001 8 8 0.0001 8 8 0.0001 8 8 0.0001 8 8 0.0001 7 1 8 8 0.00810 7 2 8 0.0550 | ODL VCENY | 248 | ∞ | | 1741 |
| K 276 8 8 0.00750 K 276 10 10 0.0750 125 8 8 0.0003 R 226 9 0.0001 R 87 10 0.0002 R 72 10 0.0010 R 97 10 0.0010 R 97 10 0.0010 237 8 0.0510 288 9 0.0550 | JUL VQENYLEY | 248 | = | | 1742 |
| K 276 8 8 0.0750 125 8 8 -0.0003 R 226 9 0.0220 R 88 9 9 0.0001 R 87 10 0.0002 R 72 10 0.0910 R 237 8 8 0.0550 | VPGSDPACY | 260 | 01 | | 1743 |
| K 276 10 0.0750 125 8 -0.0003 70 8 8 -0.0220 126 9 0.0001 127 10 0.0001 128 87 10 0.0002 129 8 0.0550 129 8 0.0550 | SALIETSY | 276 | ∞ | | 1744 |
| 125 8 -0.0003 70 8 8 0.0220 8 8 9 0.0001 8 87 10 0.0002 72 10 0.0910 74 8 8 0.0550 75 237 8 0.0550 | CALIETSYVK | 276 | 10 | 0.0750 | 1745 |
| R 226 9 0.0220 R 88 9 9 0.0001 R 87 10 0.0002 R 237 8 8 0.0550 290 9 0.0550 | CAREPUTK | 125 | ∞ | -0.0003 | 1746 |
| 226 9 0.0220 88 9 0.0001 69 9 0.0001 72 10 0.0002 237 8 0.0810 74 8 0.0550 | FSTTINY | 20 | ∞ | | 1747 |
| 88 9 0.0001 69 9 0.0001 72 10 0.0910 73 8 0.0810 74 8 0.0550 290 9 | MLEVFEGR | 226 | 6 | 0.0220 | 1748 |
| 87 10 0.0002 72 10 0.0910 237 8 0.0810 74 8 0.0550 281 8 | SNOEEEGPR | | 6 | 0.0001 | 1749 |
| 87 10 0.0002 72 10 0.0910 237 8 0.0810 74 8 0.0550 280 9 | SYSTEM | 66 6 | 6 | • | 1750 |
| 237 8 0.0910 74 8 0.0550 290 9 | SSNCEECPR | 8/ | 10 | 0.0002 | 1751 |
| 237 8 0.0810 74 8 0.0550 1 290 9 | STINTIEWE | 77 | 2, | 0.0910 | 1752 |
| 290 9 0.0330 | TINYTI WE | 757 | ×0 0 | 0.000 | 56/1 |
| 28 | III I I CMIN | 29, | 0 0 | 0.00.0 | 1755 |
| | ISYVKVLH | 281 | <i>L</i> ∞ | | 1756 |

| | | Table XVII A | | |
|-------------|----------|---|--------|------------|
| - | | Mage 2 All Motif Peptides with Binding Data | g Data | |
| edneuce | Position | No. of Amino Acids | A*1101 | SEQ ID NO. |
| SYVKVLHH | 281 | 6 | 9900:0 | 17571 |
| TINYTLWR | 73 | 6 | 1.1000 | 1758 |
| IFSKASEY | 149 | 6 | 0.0330 | 1759 |
| TCLGLSY | 179 | œ | • | 1760 |
| VEVVPISH | 991 | 6 | 0.0100 | 1761 |
| VEVVPISHLY | 991 | | | 1762 |
| VPISHLY | 691 | -∞ | | 1763 |
| /GPRALIETSY | 273 | == | | 1764 |
| ILVTCLGLSY | 176 | = | | 1765 |
| VKVLHHTLK | 283 | 01 | 0.0160 | 1766 |
| | | | | |

| | A | Table XVII B Mage 3 A11 Motif Peptides with Binding Data | Data | |
|--------------------------|-------------|--|---------|------------|
| Sequence | Position | No. of Amino Acids | A*1101 | SEQ ID NO. |
| ACYEFLWGPR | 267 | 10 | 0.0035 | 1921 |
| ALSRKVAELVH | 801 | = | | 1768 |
| ALVETSYVK | 777 | 6 | 0.1700 | 1769 |
| ASSLPTIMNY | 89°. | 01 | 0.0330 | 1770 |
| AICLGLSY | 179 | ∞ (| | 1221 |
| DSILGOPA | 730 | × × | -0.0003 | 1772 |
| DSILGUPAA EDSII GDBV | 736 | 5 6 | -0.0002 | 1773 |
| EDSILGOLN FOST GORK | 233 | λ · | 0.0002 | 4//) |
| EFOALSR | £ 5 | ⊇ ∝ | 0.0002 | 6771 |
| EFOAALSRK | 101 | . 0 | 0 0001 | 7771 |
| EGDCAPEEK | 212 | . 6 | 0.0001 | 1778 |
| ELMEVDPIGH | 165 | 10 | 0.0002 | 1779 |
| ELSVLEVFEGR | 224 | = | 0.0023 | 1780 |
| ELVHFLLLK | 115 | 6 | 0.0011 | 1781 |
| ELVHFLLLKY | 115 | 01 | 0.0003 | 1782 |
| ELVHFLLLKYR | 115 | | 0.0031 | 1783 |
| ESEFQAALSR | 102 | 01 | 0.0002 | 1784 |
| ESEFQAALSRK | 102 | = ' | 0.0004 | 1785 |
| EISYVKVLH | 280 | 6 | | 1786 |
| EISTVALER | 780 | ⊇ (| 0000 | /8/1 |
| EATCH GILSY | 2.2 | , o | 60000 | 1789 |
| FPPVIESK | 146 | · • | 100.0 | 1790 |
| FLLLKYRAR | 119 | 0 | | 1791 |
| FVQENYLEY | 250 | . 6 | | 1792 |
| FVÕENYLEYR | 250 | , 01 | 0.0012 | 1793 |
| GASSLPTTMNY | 19 | | | 1794 |
| GDCAPEEK | 213 | 80 | | 1795 |
| GDNQIMPK | 161 | ∞ | | 1796 |
| GDPKKLLTQH | 240 | 01 : | 0.0002 | 1797 |
| GGPHISY PPLH | 667 | =: | 0.00 | 1798 |
| GSVVGNWOY | 137 | _ 0 | 0.0370 | 0081 |
| HCKPEEGLEAR | 6 | ` [| | 1801 |
| HFLLLKYR | 118 | ∵ ∞ | | 1802 |
| HFLLLKYRAR | 81. | 10 | 0.0002 | 1803 |
| HFVQENYLEY | 249 | 02: | | 1804 |
| HFVQENYLEYK | 249 | 6 | | 1805 |
| HIST FFLH HMVK ISGGPH | 98 <i>7</i> | * = | | 1806 |
| IFATCLGLSY | 12. | 2 5 | 0 0004 | 1808 |
| IIVLAIIAR | 203 | ? 6 | 0.0011 | 1809 |
| ISGGPHISY | 293 | 6 | 0.0002 | 0181 |
| IVLAIIAR | 204 | ∞ : | 0.0037 | 181 |
| KVI HHMVK | 286 | ⊇ ∝ | 0.0190 | 1813 |
| |) 1 | , | , | • |

| | | Table XVILB Mage 3 A 11 Motif Pentides with Binding Data | ata ata | |
|--------------------------|-------------------|--|------------|------------|
| | Position | No. of | 1011** | ON CI COS |
| ochneuce | Control | Amino Acids | V. 1101 | SEQ ID NO. |
| GDNOIMPK | 180 | o | | 1814 |
| LGDPKKLLTQH | 239 | `= | | 1815 |
| LGSVVGNWQY | 136 | 10 | 0.0012 | 1816 |
| LIIVLAIIAR | 202 | 01 | 0.0021 | 1817 |
| CLGDNQIMPK | 189 | 01 | 0.0110 | 1818 |
| LLIIVLAIIAK | 107 | | 0.0056 | 6181 |
| CLLKYKAK TOHEVOENIX | 120 | ∞ ; | -0.0004 | 1820 |
| LEIONE VORT | 243 | _ < | | 1821 |
| LMEVDFICH MEVDPIGHI V | <u>8</u> <u>7</u> | φ <u>:</u> | 0.000.0 | 1822 |
| SRKVAELVH | 00 | <u> </u> | 0 0000 | 1823 |
| LSVLEVFEGR | 225 | 2 0 | 0.0030 | 1825 |
| LTQHFVQENY | 246 | 01 | 0.0002 | 1826 |
| LVÈTSYVK | 278 | ? ∞ | 0.0014 | 1827 |
| VETSYVKVLH | 278 | · = | | 1828 |
| LVHFLLLK | 116 | ∵ ∞ | 0.1500 | 1829 |
| LVHFLLLKY | 116 | 6 | 0.0100 | 1830 |
| LVHFLLLKYR | 116 | 10 | 0.0022 | 1831 |
| MLGSVVGNWQY | 135 | == | | 1832 |
| MNYPLWSQSY | 75 | 01 | 0.0002 | 1833 |
| MVKISGGPH | 290 | 6 | 0.0002 | 1834 |
| PACYEFLWGPR | 266 | = | -0.0002 | 1835 |
| PGSDPACY | 262 | ∞ | | 1836 |
| PLEQKSQH | 77 | ∞ : | | 1837 |
| PLEQRSQHCK | 2 | 10 | 0.0002 | 1838 |
| PLHEW VLK | 303 | ∞ ; | -0.0003 | 1839 |
| AVIOSDIACI BALVETSA | 200 | 0, | | 1840 |
| NALVEIST PATVETENNIV | 9/7 | ∞ ; | | 1841 |
| AALVEISIVA PABEDVTV | 9/7 | 01 | 0.110 | 1842 |
| SGGPHISY | 294 | • | -0.0003 | 1043 |
| SHIGDPKK | 237 | ∞ ∝ | 0.0012 | 5781 |
| SLPTTMNY | 202 | ∞ ∝ | 7 00:0 | 1846 |
| SSLPTTMNY | 69 | » 6 | | 1847 |
| SVLEVFEGR | 226 | , 6 | 0.1400 | 1848 |
| SVVGNWQY | 138 | 8 | | 1849 |
| FMNYPLWSQSY | 74 | = | | 1850 |
| rsyvkvlh | 281 | 8 | | 1821 |
| ISYVKVLHH | 281 | 6 | 0.0066 | 1852 |
| VAELVHFULLK | 113 | = ' | 0.0011 | 1853 |
| VDFIGHLY VI EVEEGE | 169 111 | ~ | 3000 0 | 1854 |
| WGPRAI VETSV | 273 | o = | 0.000.0 | 1855 |
| YFFPVIFSK | 145 | Ξ <i>σ</i> | 0.0270 | 1857 |
| VIFATCLGLSY | 176 | | | 858 |
| YVKVLHHMVK | 283 | | 0.0061 | 1859 |
| | | | | |

| | | Table XVIII A Mage 2 424 Madis Postidas with Binding Date | nding Data | |
|-------------|----------|---|------------|-----------|
| Sequence | Position | No. of Amino Acids | A*2401 . | OI ČEĆ ID |
| CVEELWGPBAI | 348 | | 0000 | 701 |
| EFI.WGPRAL | 270 | _ 0 | 90000 | 981 |
| EFLWGPRALI | 270 | \ <u>0</u> | 26000 | 186 |
| EYLOLVFGI | 156 | ? 0 | 3 5000 | 981 |
| IFSKASEYL | 120 | , 6 | 0.0230 | 186 |
| IFSKASEYLQL | 150 | = | 0.0950 | 186 |
| IWEELSML | 221 | & | 0.0007 | 186 |
| IWEELSMLEVF | 221 | = | 0.0170 | .981 |
| KMVELVHF | 112 | ∞ | 0.0005 | 186 |
| KMVELVHFL | 112 | 6 | | 981 |
| KMVELVHFLL | 112 | 01 | | 187 |
| KMVELVHFLLL | 112 | = | | 187 |
| LMQDLVQENYL | 246 | == | | 187 |
| LWGPRALI | 272 | ∞ | 0.1200 | 181 |
| LYILVTCL | 175 | ∞ | 0.0086 | 181 |
| LYILVTCLGL | 175 | 01 | 0.0140 | 187 |
| MFPDLESEF | 97 | 6 | 0.0140 | 187 |
| RMFPDLESEF | 96 | 01 | 0.0016 | 187 |
| SFSTTINYTL | 70 | 10 | 0.0150 | 187 |
| SFSTTINYTLW | 70 | = | 0.0280 | 187 |
| SYPPLHERAL | 300 | 01 | 0.0003 | 881 |
| SYVKVLHHTL | 282 | 01 | 0.1600 | 188 |
| VFAHPRKL | 238 | ∞ | 0.0005 | 88 |
| VFAHPRKLL | 238 | . 6 | 9000'0 | 188 |
| VFEGREDSVF | 230 | 01 | 0.0004 | 188 |
| VMPKTGLL | 195 | ∞ . | -0.0004 | 881 |
| VMPKIGLLI | 561 | 6: | 0.2300 | 88. |
| VMFKIGLEII | <u>c</u> | 10 | 0.0580 | 881 |

| | | Table XVIILB Mage 3 A24 Motif Peptides with Binding Data | inding Data | |
|------------|----------|--|-------------|------------|
| neuce | Position | No. of Amino Acids | A*2401 | SEQ ID NO. |
| EFLWGPRAL | 268 | = | 0 0004 | 1888 |
| WGPRAL | 270 | : 6 | 90000 | 1889 |
| TGSVVGNW | 134 | .01 | 0.0017 | 1890 |
| VOENYL | 249 | . ∞ | -0.0004 | 1881 |
| IVKISGGPHI | 289 | . = | | 1892 |
| TCLGL | 177 | . 🛇 | 0.0120 | 1893 |
| KASSSL | 150 | 6 | 0.0160 | 1894 |
| KASSSLQL | 150 | | 0.0910 | 1895 |
| KAGLL | 195 | 8 | | 9681 |
| KAGLLI | 195 | 6 | 0.4200 | 1897 |
| PKAGLLII | 195 | 01 | 0.0500 | 1898 |
| EELSVL | 221 | ∞ | -0.0004 | 1899 |
| EELSVLEVF | 221 | = | 0.0260 | 1900 |
| EVDPIGHL | 991 | 01 | | 1901 |
| IFATCL | 175 | 8 | 0.0140 | 1902 |
| IFATCLGL | 175 | 01 | 0.0480 | 1903 |
| /QYFFPVI | 142 | . 6 | 0.5300 | 1904 |
| /QYFFPVIF | 142 | 10 | 0.0170 | 1905 |
| FFPVIF | 144 | ∞ | 0.1200 | 1906 |
| DCLLGDNQI | 185 | = | 0.0026 | 1907 |
| PPLHEW | 300 | 8 | 0.0420 | 1908 |
| PPLHEWVL | 300 | 01 | 0.5900 | 6061 |
| DLESEF | 97 | 6 | 0.0049 | 1910 |
| EGREDSI | 230 | 6 | -0.0004 | 1161 |
| EGREDSIL | 230 | 01 | -0.0005 | 1912 |
| | | | | |

| | DR5w12 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|--|-------------------------|-----------------|-----------------|--------------------------------------|-----------------|-----------------|-----------------|---------------------------------------|------------------|-----------------|-----------------|-----------------|--------------------------------------|---------------------|----------------|-----------------|-----------------|----------------|-----------------|--|----------------|----------------|----------------|----------------------------------|----------------|-----------------|-----------------|------------|-----------------|-----------------|-----------------|-------------------------------------|-------------------|-----------------|-----------------|-----------------|-----------------|--|---------------------|-----------------|-----------------|--|
| | DR5w11 | | | | | | | 0.0270 | | | | -0.0005 | | | | | | | 0000 | -0.0005 | | | | | | | | | | | | | | | | | | | | | | |
| | DR4w15 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ng Data | DR4w4 | -0.0032 | -0.0032 | | | | -0.0032 | 0.1600 | | | | 0.0070 | -0.0032 | | | | | | 0 | 0.03/0 | 200 | 0.0051 | 0.0120 | | | | -0.0032 | | | | | | | | | | -0.0032 | | | | | |
| with Bindi | DR3 | 0 1400 | 0.1400 | 0.0130 | | | | 0.0113 | | | | 0.0036 | | | | 0.0660 | | | 000 | 0.0025 | | | | | | | | | | | 6000 | 0.0072 | | 0.1500 | | | | | | | | |
| Mage 2 DR Super Motif Peptides with Binding Data | DR2w2B2 | | | | | | • | 1.0000 | | | | 0.0009 | | | | | | | | -0.0022 | | | | | | | | | | | | | | | | | | | | | | |
| uper Moti | DR2wB1 | | | | | | | 0.0620 | | | | 0.0046 | | | | | | | | 0.003/ | | | | | | | | | | | | | | | | | | | | | | |
| ige 2 DR S | DR1 | 0.0330 | -0.0005 | | | | -0.0003 | 1.2000 | | | | 0.0084 | 0.0100 | | | | | | | 0.0120 | | 0.0120 | 0.0086 | | | | 0.0019 | | | | | | | | | | 0.0008 | | | | | |
| Ma | / Position n | 24 | 189 | 220 270 | 221 | 255 | 298 | ₹ \$ | 148 | 149 | 22 | 165 | 707 | 921 | 991 | 210 | 205 | 174 | 134 | € 5 | 8 | 204 | 203 | £ 29 190 | 47 | 115 | 195 | 6 | 108 | 146 | 250 | 101 | 0/7 | 245 | 175 | 44 | 501 | 0 9 | 163 | 12 | 224 | |
| Table XIX A 1 | Exemplary SeqID Num | 1913 | 1915 | 1916 | 1918 | 1919 | 1920 | 1921 | 1923 | 1924 | 1925 | 1926 | 1761 | 1929 | 1930 | 1631 | 1932 | 1933 | 1934 | 1936 | 1937 | 1938 | 1939 | 1940 | 1942 | 1943 | 1944 | 1946 | 1947 | 1948 | 1949 | 1950 | 1957 | 1953 | 1954 | 1955 | 1956 | 1058 | 1959 | 1960 | 1961 | |
| Tabl | رد. | ALGLVGAOAPATEEO | DGLLGDNOVMPKTGL | EEKIWEELSMLEVFE FFI WGPRAI IFTSYV | EKIWEELSMLEVFEG | ENYLEYROVPGSDPA | EPHISYPPLHERALR | ESEFUAAISKKM VEL FVTI GFVPA ANSPSP | FFPVIFSK ASEVLOL | FPVIFSKASEYLOLV | GEALGLVGAQAPATE | GIEVVEVVPISHLYI | GLLIIVLAIIAIEGU UEI 11 KVDADEDVTV | HI VII VTCI GI SVDG | EVVEVVPISHLYIL | IIAIEGDCAPEEKIW | IIVLAIIAIEGDCAP | SHLYILVTCLGLSY | KAEMLESVLRNCODF | N I GELLII VEAII AUE I GEVPAADSPSPPHS | GLVGAQAPATEEQQ | IIVLAIIAIEGDCA | LIIVLAIIAIEGDC | LKYKAKEPVIKAEM OLVEGIEVVEVVPI | VEVTLGEVPAADSP | MVELVHFLLLKYRAR | NOVMPKTGLLIIVLA | DLESEFOAAI | OAAISRKMVELVHFL | ODFFPVIFSKASEYL | ODLVOENYLEYROVP | OLVFGIEVVEVVPIS PATTETSVVKVI HHT | REDVIKAEMI ESVI R | RKLLMODLVOENYLE | SHLYILVTCLGLSYD | SSTLVEVTLGEVPAA | FGLLIIVLAIIAIEG | VELVHILLINI KAKE VEVAVDISHI VII VTC | VEC VI ISHETILE VIC | VVPISHLYILVTCLG | WEELSMLEVFEGRED | |
| | D Exemplary Sequence | ALGLW | DOLLG | EEKIWI FFI WG | EKIWEI | ENYLE | EPHISY | FVTI | FFPVIE | FPVIFSI | GEALG | GIEVVE | | N II A | IEVVEV | IIAIEGD | IIVLAII | ISHLYII | KAEML | LGEVP | LGLVG. | LIIVLAI | LLIIVL | LOLVEGI | LVEVTI | MVELV | NOVME PDV113 | PRMFPDI | OAAISF | ODFFP | ODLVO | PALVEG | REPVT | RKLLM | SHLYIL | SSTLVE | TGLLIIV | VELVE | VEGIEV | VVPISH | WEELS | |
| | Core SeqID Num | 2044 | 2046 | 2047 | 2049 | 2050 | 2051 | 7027 2023 | 2054 | 2055 | 2056 | 2057 | 2028 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2067 | 2068 | 2069 | 2070 | 2072 | 2073 | 2074 | 2075 | 2070 | 2078 | 2079 | 2080 | 2081 | 2087 | 2084 | 2085 | 2086 | 2087 | 2080 | 2090 | 2091 | 2092 | |
| | Core Sequence | LVGAOAPAT | LGDNOVMPK | IWEELSMLE WGPRALIFT | WEELSMLEV | LEYROVPGS | ISYPPLHER | GEVPADS | VIFSKASEY | IFSKASEYL | LGLVGAQAP | VVEVVPISH | IIVLAIIAI | II VTCI GI S | VEVVPISHL | IEGDCAPEE | LAIIAIEGD | LYILVTCLG | MLESVLRNC | VPAADSPSP | VGAQAPATE | VLAIIAIEG | IVLAIIAIE | YKAKEPVIK | VTLGEVPAA | LVHFLLLKY | MPKTGLLII | FPDLESEFO | ISRKMVELV | FPVIFSKAS | VOENYLEYR | FGEVVEVV | VTKAFMI ES | LMODLVOEN | YILVTCLGL | LVEVTLGEV | LIIVLAIIA | VPICLLN I R | IEVVEVVPI | ISHLYILVT | LSMLEVFEG | |

| Once Conce SaliD Esemplaty Besmplaty DR6A019 DR5A2 DR5A Sociation Num Sequence Core SaliD Esemplaty DR6A01 DR5A2 DR5A DR5A2 SEYDGLIGNEY 1913 | | | Table XIX A 2 | KA2 | Mage 2 DR Su | oer Motif Peptic | Mage 2 DR Super Motif Peptides with Binding Data | | |
|--|-------------------|-------------------|---|------------------------|--------------|------------------|--|-----|-------|
| 2944 ALGLVGAQAPATEEQ 1913 -0.0011 2945 CLGLSYPGALGONQY 1914 -0.0011 2945 CLGLSYPGALGONQY 1915 2946 EKIWPELSMLEYFE 1916 -0.0011 2048 EKIWPELSMLEYFE 1916 -0.0011 2048 EKIWPELSMLEYFE 1917 -0.0011 2059 EKIWPELSMLEYFE 1917 -0.0011 2051 EPHTATERQYPGSDPA 1920 2051 EPHTATERGYPGARANER 1920 2052 EFICAARSENOL 1922 2053 EPHTATERGYPGARANER 1922 2054 FFIVIERGARFAULT 1922 2055 EFICAARSENOL 1922 2056 GEALGLYGAQAPATE 1922 2056 GEALGLYGAQAPATE 1922 2056 GEALGLYGAQAPATE 1922 2056 GEALGLYGAQAPATE 1932 2057 LLINTALAIRGEDCAP 1933 2057 GLYGGACAPATEQQ 1937 2056 GALGLYGACAPATEQQ 1937 2057 LLINTALAIRGEDCA 1934 2057 REVELINGULYAR 1934 2057 RALLINGULYGENAPH 1935 2057 RALLINGULYGENAPH 1935 2058 RELLINGULYGENAPH 1935 2058 RELLINGULYGENAPH 1935 2059 VERFURKAREE 1935 2050 VERFURK | Core Sequence | Core SeqID Num | Exemplary Sequence | Exemplary SeqID Num | DR6w19 | DR7 | DR8w2 | DR9 | DRw53 |
| 265 CLULATIVALIDAÇA 1914 -0.0011 2045 CLULATIVALIDAÇA 1914 -0.0011 2045 ERKIWEELSMALEYEE 1916 -0.0011 2045 ERKIWEELSMALEYEE 1916 -0.0011 2045 ERKIWEELSMALEYEE 1917 -0.0011 2055 ERKIWEELSMALEYEE 1917 -0.0067 -0.100 2055 ERFICENTANISPER 1922 -0.0011 2055 ERFICENTANISPER 1922 -0.0011 2055 ERFICENTANISPER 1922 -0.0011 2055 ERFICENTANISPER 1925 -0.0011 2055 ERFICENTANISPER 1925 -0.0011 2055 ERFICENTANISPER 1925 -0.0011 2055 ERFICENTANISPER 1925 -0.0011 2055 ERFICENTANISPER 1926 -0.0011 2055 ERFICENTANISPER 1926 ERFICENTAN | LVGAQAPAT | 2044 | ALGLVGAQAPATEEQ | 1913 | | -0.0011 | | | |
| 2047 BEKIWEELSMLEYPE 1916 2048 ERIWEELSMLEYPE 1917 2059 ENTLEPROPALIETSY 1917 2051 ENTLEPROPALIETSY 1917 2052 ESEPGAAISKWHE 1921 0.0067 0.5100 2053 ESEPGAAISKWHE 1922 0.0067 0.5100 2054 FPIVIESKASEVLQLV 1922 2055 EVICETRANASEPP 1922 2056 GPALGINGAGAAFE 1922 2057 GIEVVEVPRISHLYT 1926 2058 GPALGINGAGAAFE 1922 2059 HFILLKYRAREPWK 1928 2059 HFILLKYRAREPWK 1931 2059 HTILLKYRAREPWK 1931 2050 LGEVPAAISEPPH 1931 2051 LGEVPAAISEPPH 1931 2052 LGEVPAAISEPPH 1935 2054 LGEVPAAISEPPH 1934 2055 HTILLKYRAREPWK 1934 2056 KTGLIINTAINGEDCA 1939 2057 LGEVPAAISEPPH 1934 2057 LGEVPAAISEPPH 1934 2057 LGEVPAAISEPPH 1934 2057 LGEVPAAISEPPH 1934 2057 LGEVPAAISEPPH 1935 2057 LGEVPAAISEPPH 1935 2057 LGEVPAAISEPPH 1935 2057 LGEVPAAISEPPH 1935 2057 REMERIVARIETYRA 1935 2058 REPVIRENCENTRE 1935 2058 REPVIRENCENTRE 1935 2058 REVYRENCENTRE 1935 2059 VVPISHLYILLKYRARE 1935 2059 VVPISHLYILLYTE 1935 2059 VVPISHLYILTE 1935 2059 VVPISHLYILLYTE 1935 2059 VVPISHLYILTE 1935 2059 VVPISHLYILLYTE 1935 2059 VVPISHLYILLYTE 1935 2059 VVPISHLYILLYTE 1935 2059 VVPISHLYILLYTE 1935 2059 VVPISHLYILTE 1935 2059 VVPISHLYILLYTE 1935 2059 VVPISHLYILTE 1935 2050 VVPISHLYILTE 1 | GDNQVMPK | 2046 2046 | DGLLGDNQVMPKTGL | 1914 1915 | | -0.0011 | | | |
| 2049 EKIWEELSMLEVFEC 1918 2050 ENTLEPRQVPGSDPA 1919 2051 ENTLEPRQVPGSDPA 1920 2052 ESEPGAALISKMYEL 1921 0.0067 2053 EPHUSPRADSPP 1922 0.5100 2054 EPHUSPRADSPP 1922 0.5100 2055 GEALGLYCAGAART 1923 0.0710 0.0900 2056 GEALLINCAGAGATE 1923 0.0710 0.00011 2057 GELLINCAGAGATEL 1923 0.0710 0.0011 2058 HFILLLXYRAREBYTK 1932 0.0711 0.0011 2059 HFILLLXYRAREBEYK 1932 0.0011 0.0011 2066 IEVVEVYPISHATU 1933 0.0011 0.0011 2067 IEGCVAPADSEPHIS 1933 0.0011 0.0011 2066 IEVVEVYPISHATU 1934 0.0011 0.0011 2067 IECVPAPADSEPHIS 1934 0.0011 0.0011 2066 KYGLINGDLVQENYTEL 1944 0.0011 | ELSMLE PRALIFT | 2047 2048 | EEKIWEELSMLEVFE FFI WGPRAI IFTSYV | 1916 | | | | | |
| 2050 ENYLEYRQVPGSDPA 1919 -0.0011 2051 ENYLEYRQVPGSDPA 1919 -0.0011 2053 ESFQARISKAMEL 1920 -0.0011 2054 ESFQARISKAMEL 1922 0.5100 2055 GEALGUVGAQAPTE 1923 0.5100 2056 GEALGUVGAQAPTE 1925 0.0710 0.00011 2057 GILUTALAIMEGD 1922 0.0011 0.0011 2058 GILUTALAIMEGD 1923 0.0011 0.0011 2059 HYLLYKYRAREPYTK 1928 0.0011 0.0011 2060 HYLLIATGGLSYDG 1933 0.0011 0.0011 2060 HYLLIATGGLSYL 1933 0.0011 0.0012 2061 HYLLIATGGLSYL 1933 0.0011 0.0012 2062 LITAYAIMEGDC 1934 0.0012 0.0120 2070 LLIAYAAREPYTKAEM 1941 0.0012 0.0012 2071 LUKYTGGLVAYAE 1945 0.0011 0.0012 <t< td=""><td>WEELSMLEV</td><td>2049</td><td>EKIWEELSMLEVFEG</td><td>1918</td><td></td><td></td><td></td><td></td><td></td></t<> | WEELSMLEV | 2049 | EKIWEELSMLEVFEG | 1918 | | | | | |
| 2053 EPHISYPPHEAALR 1920 -0.0011 2053 ESTEVARANEANER 1922 -0.00011 2054 EVIT, GEVPAADSPEP 1922 -0.00011 2055 GEALGU VGAQAATE 1923 -0.0011 2056 GEALGU VGAQAATE 1923 -0.0011 2057 GELIJIVALIAEGU 1923 -0.0011 2059 GLIJIVALIAEGU 1923 -0.0011 2059 GLIJIVALIAEGU 1923 -0.0011 2050 H.YILVTRAREPYTK 1933 -0.0011 2061 H.YILVTRAREPYTK 1933 -0.0011 2062 H.YILVTRAREPYTK 1933 -0.0011 2063 H.YILVTRAREPYTK 1933 -0.0011 2064 H.YILVTRAREPYTK 1933 -0.0011 2065 H.YILVTRAREPYTK 1933 -0.0011 2066 H.YILVTRAREPYTK 1934 -0.0011 2067 LIJIVALIAEGUC 1939 -0.0013 2067 LIJIVALIAEGUC 1939 -0.0013 2071 LILVTRAREPYTKAEM 1941 -0.0011 2072 LIJIVALIAEGUC 1938 -0.0013 2073 LIJIVALIAEGUC 1939 -0.0013 2074 NYELVRAREPYTKAEM 1944 -0.0011 2075 LIJIVALIAEGUC 1938 -0.0013 2076 RAMEDLESERQAL 1946 -0.0011 2077 LIJIVALIAEGUC 1938 -0.0013 2077 RAMEDLESERQAL 1946 -0.0011 2078 RAMEDLESERQAL 1946 -0.0011 2079 QDLVQERVLEYROP 1949 -0.0011 2070 QDLVQERVLEYROP 1945 -0.0011 2080 REPYTKAEMLESVYE 1955 -0.0011 2081 REPYTKAEMLESVYE 1955 -0.0011 2082 STILVEYTLGEVPA 1945 -0.0011 2083 VELLIMALIKE 1955 -0.0011 2084 VELLIMALIKE 1955 -0.0011 2085 VELLIMALIKE 1955 -0.0011 2095 VERLIMALIKE 1955 -0.0011 2097 VERLIMALIKE 1955 -0.0011 | LEYRQVPGS | 2050 | ENYLEYRQVPGSDPA | 6161 | | | | | |
| 2052 ESET (ÇALINARAM PLE 2054) 2054 FEPUÇARA SERVEL 1922 2055 FEPUÇARA SERVEL 1922 2056 GEALGL VGAQAPATE 1922 2057 GELLIVARA LEDY 1924 2058 GEALGL VGAQAPATE 1925 2059 HFLLLKYRA REPYTK 1928 2060 HLYLLYRYA REPYTK 1939 2061 HLYLLYRYA REPYTK 1939 2063 HFLLLKYRA REPYTK 1939 2064 HLYLLYRYA REPYTK 1931 2065 KARALL ESVLANCODE 1935 2065 KARALL ESVLANCODE 1935 2066 KTGLLINVAIIALE 1935 2067 LGEVPAAD SPSPHS 1935 2068 KTGLLINVAIIALE 1935 2069 LGLVGAQAPATEEQQ 1935 2060 LLIVA ALIA REDCCAP 1935 2060 LLIVA ALIA REDCCAP 1935 2070 LLIVA ALIA REDCCAP 1935 2071 LGLVGAQAPATEEQQ 1937 2071 LGLVGAQAPATEEQQ 1937 2072 LGLVGAQAPATEEQQ 1937 2073 LVGTLGEVVEVYPR 1945 2074 NVELVHELLYRYA 1945 2075 LGLVGGEVPANDSP 1940 2076 PRELLINVAINT 1945 2076 QULVGERVVEVYPR 1947 2077 QAARSK RWYLLYHT 1947 2078 QULVGERVVEVYPR 1947 2078 QULVGERVVEVYPR 1945 2078 GEPVTKA REPYTKA REPTYPR 1947 2078 QULVGERVYEVYPR 1945 2078 CALLINVAINT 1951 2078 KALLETSV WYLHT 1951 2078 KALLETSV WYRSH 1945 2078 VELVHFLLK YRARE 1955 2079 VERSWALLY YRARE 1955 2079 VERSWALLY YRA REPTER 1955 2079 VERSWALLY YRA REPTER 1955 2079 VERSWALLY YRA REPTER 1955 2070 VERSWALLY YRA REPTER 1955 | PLHER | 2051 | EPHISYPPLHERALR | 1920 | 17000 | -0.0011 | 0.00 | | |
| 2054 FFPVIESKASEYLQL 1922 2055 FFPVIESKASEYLQL 1924 2065 FFPVIESKASEYLQL 1925 2057 GIEVVEVVPISHLYI 1926 2057 GIEVVEVVPISHLYI 1926 2058 GILLINALIAREDD 1929 2066 HEYLLKYRREPYTR 1930 2066 HEYLLKYRREPYTR 1931 2066 HEYLLKYRREPYTR 1931 2066 HEYLLKYRREPYTR 1932 2065 INLEGDCAPERIUM 1931 2066 KARLALAGEGCAP 1932 2066 KARLALAGEGCAP 1933 2067 KARLALAGEGCAP 1935 2068 LIATULIALAGEGCA 1936 2068 LIATULIALAGEGCA 1936 2071 LLIVALIALEGCA 1939 2072 LQLVGAQAPATEQQ 1937 2073 LULYALIAGEGCA 1939 2074 LLIVALIAGEGCA 1939 2075 LQLVGETVPRAPPT 1941 2075 RQVARFTCLLIVARA 1944 2077 RKLLMODLYGENYL 1945 2077 RALETSYRKALH 1945 2077 RALETSYRKALH 1945 2077 RALETSYRKALH 1945 2078 RKLLMODLYGENYL 1945 2079 QDLVGETVEVPRAPPT 1945 2079 QDLVGETVEVPRAPPT 1955 2080 QLVGTGEVPRAPPT 1955 2080 GLTLINALIALEGT 1955 2080 VECHYRALEGT | VPAADS | 2027 | ESEF (JAAISKKIM VEL FVTI GFVPA A DSPSP | 1921 | 0.006/ | 0.5100 | 0.0310 | | |
| 2055 FEVIFSKASEVLQLV 2056 GEALGLAGAQAPATE 2057 GELGLAGAAPATE 2058 GELGLAGARAPATE 2059 GELGLAGARAPATE 2059 GELGLAGARAPATE 2059 GELGLAGARAPATE 2059 HTLLLKYRAREPYTK 2060 HEVVEVYRSHLYI 2061 INTEGDCAPEKTW 2063 INTARIANGEDCAP 2064 ISHATILYTCLGLSY 2065 INTARIANGEDCAP 2065 INTARIANGEDCAP 2066 KYGLLINVARIAE 2066 KYGLLINVARIAE 2066 KYGLLINVARIAE 2066 KYGLLINVARIAE 2066 KYGLLINVARIAE 2066 KYGLLINVARIAE 2067 LGLVGAQAPATEGQQ 2070 LLIVARIAEGDCA 2071 LLIVARIAEGDCA 2071 LLIVARIAEGDCA 2071 LLIVARIAEGDCA 2071 LLIVARIAEGDCA 2071 MVPRYGLLIVA 2072 LQLVGREVVPY 2073 LYGURVEVYP 2073 LYGURVEVYP 2074 MVELVHLLLKYRAR 2076 MVPRYGLLIVA 2077 RWLLMADLLXYRAR 2077 RWLLMADLLXYRAR 2078 RWLLMADLLXYRAR 2077 RWLTARAE 2077 RWLLMADLLXYRAR 2078 QLVGREVVEVPIS 2077 RWLTARAE 2078 QLVGREVVEVPIS 2077 RWLTARAE 2077 RWLTARA | KASEY | 2055 | FFPVIFSK A SFYI OI | 1923 | | | | | |
| 2056 GEA/GL/VGA/QRÄTE 1925 0.0710 0.0900 2057 GIEVVEVVRISHLYI 1926 0.0710 0.0900 2058 GLLILKYRAREBYTK 1929 -0.0011 2050 HFLLLKYRAREBYTK 1939 -0.0011 2060 HLYILYTCLGLSYDG 1939 -0.0011 2061 IIVALAILAIGEDCAPEKIW 1931 -0.0015 2063 IIVALAILAIGEDCAPEKIW 1934 -0.0011 2064 SHELYILYALATAREDCA 1934 -0.0011 2065 KAEMLESVLRNOODF 1935 -0.0011 2066 KAGLAINALAINEDCA 1938 -0.0011 2067 LGLYGAQAPATEEQQ 1937 -0.0011 2068 LIGLYGAQAPATEEQQ 1937 -0.0011 2070 LLINAAIAIAEDCA 1938 -0.0011 2071 LLIVARAREPYTKAEM 1941 -0.0011 2072 LQLYFGIEVVEVVPI 1945 -0.0011 2073 LVEVILGEVPAADSP 1945 -0.0011 2074 QDE | FSKASEYL | 2055 | FPVIFSKASEYLOLV | 1924 | | | | | |
| 2057 GIEVVEVPISHLYI 1926 0.0710 0.0900 2058 GILLILKYRAREPTK 1928 -0.0011 2059 HFLLLKYRAREPTK 1929 -0.0011 2060 IEVVEVPISHLYIL 1930 -0.0011 2061 IEVVEVPISHLYIL 1930 -0.0011 2062 IIAEGDCAPERTK 1931 -0.0015 0.0230 2063 IIVLAIIAEGDCAP 1933 -0.0015 0.0230 2065 KAEMLESVLINCODF 1934 -0.0011 2066 LIGUVGAQAPETEQQ 1937 -0.0011 2067 LGEUVGAQAPETEQQ 1937 -0.0011 2069 LIIVLAIIAEGDCA 1938 0.01130 2060 LIIVLAIIAEGDCA 1939 -0.00130 2070 LIILKYRAREPYKRAEM 1940 -0.00130 2071 LILKYRAREPYKRAEM 1940 -0.00130 2072 LQLVGEVVEVVPI 1945 -0.0011 2073 RWIPDLESSERQAI 1946 -0.0011 2075 RWIPDLESSERQAI 1946 -0.0011 2076 RAKLLMQDLVQENYL 1945 -0.0011 2077 RWIPDLESSERQAI 1946 -0.0011 2078 QALISYKKWELVHIT 1945 -0.0011 2078 REPYTK.EMLESYT 1945 -0.0011 2078 RELINITATIOGE 1950 -0.0011 2080 VECUPISTY WALTER 1955 -0.0011 2081 REPYTK.EMLESTY 1945 -0.0011 2082 SHLTILTATIOGE 1950 -0.0011 2083 SHLTILTATIOGE 1950 -0.0011 2084 VECUPISTY WALTER 1955 -0.0011 2085 SHLTILTATIOGE 1950 -0.0011 2087 VECUPISTY WALTER 1955 -0.0011 2088 VECUPISTY WALTER 1955 -0.0011 2089 VECUPISTY WALTER 1955 -0.0011 2090 VEGUPVERLYILTCE 1955 -0.0011 2091 VERLEAGERED 1961 -0.0011 2092 VEELSMELFFERED 1961 -0.0011 2093 VEELSMELFFERED 1963 -0.0011 2094 VERLEAGERED 1964 -0.0011 2095 VEELSMELFFERED 1964 -0.0011 2096 VERLEAGERED 1964 -0.0011 2097 VERLEAGERED 1964 -0.0011 2097 VERLEAGERED 1964 -0.0011 | GLVGAQAP | 2056 | GEALGLVGAQAPATE | 1925 | | | | | |
| 2058 GLUITVAILAIREDD 1927 -0.0011 2050 HFLLLKYRAREPUTK 1938 2060 HLYILYCLGISYDG 1929 2061 IEVVEVPRISHLYIL 1930 2062 IIACECCAPEEKIW 1931 2063 IIVLAILAIGEGCAPE 2064 ISHLYILYCLGISY 1933 2065 KAEMLESVLRNCQDF 1934 2066 KTGLLIIVAILAIE 1935 0.0015 0.0120 2067 LGEVPAADSPSPPHS 1936 0.0120 2068 KTGLLIIVAILAIE 1935 0.0015 0.0130 2069 LGLVGAQAPATEGQ 1939 0.0130 2060 LLIIVAILAIAIEGDC 1939 0.0130 2072 LGLVGAQAPATEGQ 1939 0.0130 2073 LGLVGEVPAADSP 1942 2070 LLIKYRAREPUTKAEM 1941 2070 LLIKYRAREPUTKAEM 1941 2071 LLKYRAREPUTKAEM 1945 2071 LLKYRAREPUTKAEM 1945 2072 RAMEPLAIRYRAR 1945 2073 RAMPPLICKYRAR 1945 2076 QDLVGENYLE 1955 2077 RRAIPLLIKYRAR 1951 2078 QLVFGIEVVEVPRIS 1950 2078 QLVFGIEVVEVPRIS 1951 2078 RALLIKYRAEM 1952 2078 CLIIVAILGEG 1956 2078 CLIIVAILGEG 1956 2078 VEFURLLIKYRARE 1955 2078 VEFURLLIKYRARE 1955 2079 VEFURLLIKYRARE 1957 2070 VEFURLLIKYRARE 1955 2070 VEFURLLIKYRARE 1955 2071 VVPRILLIKYRARE 1955 2072 VEFURLLIKYRARE 1955 2073 VEFURLLIKYRARE 1955 2074 VFGIEVVEVPRILLIKYRARE 1955 2075 VEFURCHISTSY 1955 2076 VEFURCHISTSY 1955 2077 VPRILLIKYRARE 1955 2077 VPRILLIKYRARE 1955 2078 VEFURLLIKYRARE 1955 2078 VEFURLLIKYRARE 1955 2079 VFGIEVVEVPRILLIKYRARE 1955 2070 VFGIEVVERFILLIKYRARE 1955 2 | VVEVVPISH | 2057 | GIEVVEVVPISHLYI | 1926 | 0.0710 | 0.0900 | 0.0089 | | |
| 2009 HFLLLKYRAREPVIR, 1928 2061 IEVVEVVPISHLYIL 2063 IIALEGDCAREEKIW 2064 ISHLYILVTCLGLSY 2064 ISHLYILVTCLGLSY 2065 IIALEGDCAREEKIW 2065 IIALEGDCAREEKIW 2066 ISHLYILVTCLGLSY 2066 ISHLYILVTCLGLSY 2066 KTGLLIIVLANIANE 2066 KTGLLIIVLANIANE 2066 KTGLLIIVLANIANE 2066 LGLVAQAPATEQQ 2066 KTGLLIIVLANIANE 2067 LGLVAQAPATEQQ 2068 LGLVAQAPATEQQ 2069 LIVLANIANGDCA 2070 LLIKYRAREPVTKAEM 2071 LQLVFGTEVVVPP 2072 LQLVFGTEVVVPP 2073 LVEVTLGEVVAVPP 2073 LVEVTLGEVVAVPP 2074 RAMFPDLESEFQAAI 2075 RWAFDLESEFQAAI 2076 RAMFPDLESEFQAAI 2077 RAMFPDLESEFQAAI 2077 RAMFPDLESEFQAAI 2078 QDLVGEVVEVVPS 2080 QDLVGEVVEVVPS 2080 QDLVGEVVEVPRS 2080 QDLVGEVVEVPRS 2080 QDLVGEVVEVPRS 2080 GDLVGEVVEVPRS 2080 GDLVGEVVEVPRS 2080 GDLVGEVTAAANE 2080 GDLVGEVVEVPRS 2080 GDLVGEVVEVPRS 2080 GDLVGEVVEVPRS 2080 VFGTEVVEVPRS 2080 VFGTEVPRS 2080 VFGTEVP | AllAl | 2058 | GLLIIVLAIIAIEGD | 1927 | | -0.0011 | | | |
| 266 IIATATALLALASTUU 1929 266 IIATATALLALASTUU 1930 266 IIATATALLALASTUU 1930 266 IIATATATATATATATA 1931 266 IIATATATATATATA 1933 266 KARALESVLRINCOPF 1933 266 KARALESVLRINCOPF 1935 266 LANGENARRODE 1935 266 LANGENARRODE 1936 267 LGEVPAADSPSPHS 1936 268 LGLVGAQAPATEQQ 1937 268 LGLVGAQAPATEQQ 1938 269 LIIVAAIIATEGDCA 1938 260 LLIVAAIIATEGDCA 1939 260 LLIVAAIIATEGDCA 1939 260 LLIVAAIIATEGDCA 1939 260 LLIVAAIIATEGDCA 1939 261 LLIVAAIIATEGDCA 1940 261 LLIVAAIIATEGDCA 1940 262 LOUVEITEVVEVPP 1941 263 NAVELVHELLKYRAR 1944 264 ANSEKMANELVHEL 1945 267 QAAISRAMVELVHIT 1945 268 RALLESVVEVPPI 1945 268 RALLESVVEVPPI 1955 268 STLVEVTLGEVPAA 1955 268 STLVEVTLGEVPAA 1955 268 VEVPISILLKYRARE 1955 268 VEVPISILLKYRARE 1955 268 VEVPISILLKYRARE 1955 269 VEVPISILLKYRARE 1956 269 VEVPISILLSY 1 | YKAKEP | 2029 | HFLLLKYKAKEPVIK | 8761 | | | | | |
| 2662 IIACGOCAPEEKIW 1931 2664 ISHLYILYAZIALIK 1932 2665 KAEMILEYKRNODF 1933 2666 KTGLLINLAIIAE 1935 2666 KTGLLINLAIIAE 1935 2666 KTGLLINLAIIAE 1936 2667 LGEVPAADSPSPHS 1936 2668 LGEVPAADSPSPHS 1936 2669 LINTAIIAEGDC 1938 2670 LLIKYRAREPYTKAEM 1940 2671 LLKYRAREPYTKAEM 1941 2671 LLKYRAREPYTKAEM 1941 2671 LLKYRAREPYTKAEM 1941 2672 LAVITCGEVPAADSP 1942 2673 LVEYTLGEVPVANSP 1941 2674 MYELJMELLKYRAR 1945 2675 LVEYTLGEVPAADSP 1945 2676 AALSKWAFTGLLINTA 1946 2677 PRALLMQDLVQENYL 1946 2677 PRAKLLMQDLVQENYL 1946 2678 QAAISRKAWELWHT 1945 2678 QAAISRKAWELWHT 1951 2688 REPYTKAEMLESVLR 1955 2681 QLYGIEVVEVPIS 1956 2681 SHLYILYTCLGLSYD 1954 2682 STILVETLGEVPAAR 1955 2683 STILVILAIIAEG 1956 2693 VEVPISHLYILYTCL 1958 2694 VFGIEVVEVPISH 1951 2695 VEVPISHLYILYTCLG 1956 2695 VEFIEVWEPVRISH 1951 2695 VETPURFALESVLR 1954 2695 VETPURFALESVLR 1954 2695 VETPURFALESVLR 1954 2695 VETPURFALESVLR 1955 2695 VETPURFALESVLR 1955 2695 VETPURFALESVLR 1955 2695 VETPURFALESVLR 1954 2695 VETPURFALESVLR 1954 2695 VETPURFALESVLR 1955 2695 VETP | ICLULS Weight | 2060 | FLYSEVARICES INC | 1929 | | | | | |
| 2663 IIIVLAIDERGLAN 1932 2664 ISHLYILVTCLGLSY 1933 2665 KAEMLEVALRINCQDF 1933 2666 KTGLLIIVALAIRE 1935 2667 LGEVPAADSPSPPHS 1936 2668 LGLVGAQARTEEQQ 1937 2669 LLIIVALAIIAGGDCA 1938 2671 LLKYRAREPVTKAEM 1940 2672 LQLYGGEVPAADSP 1942 2673 LVEVTLGEVPAADSP 1942 2674 MVELVHFLLKYREM 1943 2675 LQLYGGEVPAADSP 1942 2676 MVELVHFLLKYREM 1943 2677 LLKYRAREPUTKAEM 1946 2678 MVELVHFLLKYREW 1946 2676 PRIKLIMQDLVGENYL 1946 2677 QULVGENYLVERYQYP 1949 2678 QAAISRKMVELVHHT 1951 268 RALLETSYVKVLHHT 1951 268 SSTLVEYTLGEVPAA 1952 268 SSTLVEYTLGEVPAA 1953 268 | CAPEE | 2062 | II A FEGURA PEFKIW | 1031 | | | | | |
| 2065 KAEMLESVIRNCQDF 1934 2066 KTGLIIVLAIRIAIE 1935 0.0015 0.0220 2066 KTGLIIVLAIRIAIE 1936 0.0015 0.00210 2067 LGEVPAADSPSPHS 1936 0.0015 2069 LINVAIRIEDCA 1939 0.0130 2070 LLINVAIRIEDCA 1940 2071 LLKYRAREDPYTKAEM 1941 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPAADSP 1942 2074 NQVMPKTGLLIIVLA 1944 0.0011 2075 NQVMPKTGLLIIVLA 1945 2076 RKLLMQDLVQENYL 1945 2077 RWELLMQDLVQENYL 1945 2078 QDLVGENYLESRÇAAI 1946 2077 RWELLMQDLVQENYL 1947 2078 QDLVGENYEVVPI 1945 2078 RALIETSYVKVLHHT 1951 2080 QDLVGENYLEXRQVP 1955 2080 QDLVGENYLEXRQVP 1955 2081 RKLLMQDLVQENYLE 1955 2083 REPVIKABLESVR 1955 2084 RKLLMQDLVQENYLE 1955 2085 STLVEVTLGEVPAA 1955 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLIVLAIREG 1955 2088 VEVVPISHLYILLXYRARE 1957 2089 VEVVPISHLYILLXYRARE 1957 2080 VEUVPISHLYILLXYRARE 1957 | AIFGD | 2002 | IIVI AIIAIEGDCAP | 1631 | | | | | |
| 2065 KAEMLESVLRNCQDF 1935 0.0015 0.0290 2066 KTGLIIIVLAIIAIE 1935 0.0015 0.0290 2066 LGVGAQAPATEEQQ 1936 0.0013 0.0120 2066 LIIVLAINIEGDCA 1938 0.0130 2070 LLINYARAEPUTKAEM 1940 0.0130 2071 LLEVTLGEVPAADSP 1942 -0.0011 2073 LVEVTLGEVPAADSP 1943 -0.0011 2074 MYELVHFILLIKYRAR 1943 -0.0011 2075 NQYMRYTGLIINLA 1945 -0.0011 2075 NQVMRYTGLIINLA 1945 -0.0011 2075 NQVMRYTGLIINLA 1945 -0.0011 2076 QDLVGEVVENPIL 1945 -0.0011 2077 PRMFPDLESEFQAAI 1946 -0.0011 208 QDLVGEVVENPIL 1945 -0.0011 208 QDLVGEVVENPIL 1945 -0.0011 208 QLVFGEVVENPIL 1945 -0.0011 208 STLVEVTLGEVPA | VICE | 2064 | ISHI VII VTCI GI SV | 1633 | | | | | |
| 2066 KTGLLIVLAIIAIE 1935 0.0015 2067 LGEVPAADSPSPPHS 1936 -0.0011 2068 LGLVGAQAPATEQQ 1938 -0.0011 2069 LINLAIAIAIGEGDC 1938 0.0120 2070 LLIKYRAREPVTKAEM 1940 0.0130 2071 LLKYRAREPVTKAEM 1942 -0.0011 2073 LVEVTGEVPADSP 1942 -0.0011 2074 MVELVHFLLKYRAR 1943 -0.0011 2075 MQVMFYTGLLIVLA 1946 -0.0011 2075 MQVMFFDLESEFQAAI 1946 -0.0011 2076 PRKLLMQDLVQENYL 1948 -0.0011 2077 PRWFPDLESEFQAAI 1946 -0.0011 2078 QDLVQENYLEYRQVPI 1949 -0.0011 2079 QDLVQENYLEYRQVPI 1949 -0.0011 2081 RALLIMQDLVQENYLE 1953 -0.0011 2082 RALLIMQDLVQENYLE 1953 -0.0011 2084 RKLLMQDLVQENYLE 1954 -0.0011 | SVIRNO | 2065 | KAEMI ESVI RNCODE | 1934 | | | | | |
| 2067 LGEVPAADSPSPPHS 1936 -0.0011 2068 LGLVGAQAPATEQQ 1937 -0.0120 2070 LIIVARIAIGGDC 1938 0.0130 2071 LLKYRAREPVTKAEM 1940 0.0130 2072 LQLVFGIEVVEVVPI 1941 -0.0011 2073 LVEYTGEVPAADSP 1942 -0.0011 2074 MVELVHFLLKYRAR 1944 -0.0011 2075 NQVMPKTGLLIYLA 1945 -0.0011 2076 PRKLLMQDLVQENYL 1946 -0.0011 2077 PRMFPDLESEFQAAI 1946 -0.0011 2078 QDLVQENYLEYRQVP 1949 -0.0011 2079 QDLVQENYLEYRQVP 1949 -0.0011 2080 QDLVQENYLEYRQVP 1951 -0.0011 2081 QLVFGIEVVEVPR 1952 -0.0011 2082 RALLMQDLVQENYLE 1953 -0.0011 2088 VELVHFLLLKYRARE 1957 -0.0011 2080 VELVHFLLLKYRARE 1952 -0.0011 <td>VLAII</td> <td>2066</td> <td>KTGLIJIVI.AIIAIE</td> <td>1935</td> <td>0.0015</td> <td>0 0230</td> <td>-0 0004</td> <td></td> <td></td> | VLAII | 2066 | KTGLIJIVI.AIIAIE | 1935 | 0.0015 | 0 0230 | -0 0004 | | |
| 2068 LGLVGAQAPATEEQQ 1937 2069 LINVLAIIMEGDCA 1938 2070 LLIIVLAIIMEGDCA 1939 2071 LLKYRAREPYTKAEM 1940 2073 LQLYRGIEVVEVPI 1941 2073 LQLVFGIEVVEVPI 1941 2074 MYELYHFLLKYRAR 1945 2075 MQVMPKTGLIIVLA 1945 2076 PRALPDLESEQAAI 1946 2077 PRMFPDLESEQAAI 1946 2078 QAAISRKMVELVHFL 1947 2078 QDLYQENYLEYRQVP 1949 2080 QDLYQENYLEYRQVP 1949 2081 REPVTKAEMLESVLR 1951 2082 RALIETSYVKVLHHT 1951 2083 RELLMQDLVQENYLE 1953 2084 RKLLMQDLVQENYLE 1955 2087 TGLLIIVLAIIAIGG 1956 2087 TGLLIIVLAIIAIGG 1956 2088 VELVHFLLLKYRARE 1957 2089 VEVPPISHLYILYTC 1959 2090 VFGIEVVEVVPPISHL 1959 2091 VVPRISHLYILYTC 1959 2091 VVPRISHLYILYTC 1950 2092 WEELSMLEVFGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 2095 VPFLWGPRALIETSY 1963 | ADSPSP | 2067 | LGEVPAADSPSPPHS | 1936 | | -0.0011 | | | |
| 2069 LIIVLAIIAÌEGDCA 1938 2070 LLIKYRAREPVTKAEM 1940 2071 LLKYRAREPVTKAEM 1941 2073 LVEVTLGEVPAADSP 1942 2074 MVELVHFLLKYRAR 1943 2075 MVAPKTGLLINLA 1945 2076 MVELVHFLLKYRAR 1945 2077 MVAPKTGLLINLA 1945 2077 PRMEDLESEÇAAI 1946 2078 QAAISRKMVELVHFL 1947 2078 QAAISRKMVELVHFL 1947 2079 QDEPVIFSKASEYL 1948 2070 QDEPVIFSKASEYL 1948 2070 QDEPVIFSKASEYL 1949 2081 RALIETSYYKVLHTT 1951 2082 RALIETSYYKVLHTT 1951 2083 REPVTKAEMLESVLR 1953 2083 REPVTKAEMLESVLR 1953 2084 STILVAICAGLSYD 1954 2085 STILVAICAGLSYD 1955 2087 TGLLINLAIAIGG 1956 2080 VEVPPISHLYILYTC 1959 2090 VVFGIEVVEVPRISHL 1959 2090 VVFGIEVVEVPRISHLYILYTC 1959 2091 VVPRISHLYILYTC 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 2095 VPFLWGPRALIETSY 1963 | OAPATE | 2068 | LGLVGAOAPATEEOO | 1937 | | | | | |
| 2070 LLIIVLAIIAIEGDC 1939 2071 LLKYRAREPYTKAEM 1940 2072 LQLVFGIEVVEVVP1 1941 2073 LVEVTLGEVPAADSP 1942 2074 MVELVHFLLLKYRAR 1944 2075 MQVMPKTGLLIIVLA 1945 2076 PRKLLMQDLVGENYL 1946 2077 PRMFDLESEFQAAI 1946 2077 PRMFDLESEFQAAI 1946 2079 QDFPVIFSKASEYL 1947 2080 QDLVGENYEFKQVP 1949 2081 RALIETSYVKVLHFT 1951 2082 RALIETSYVKVLHFT 1951 2083 REPVTKAEMLESVLR 1953 2083 REPVTKAEMLESVLR 1953 2084 KKLLMQDLVQENYLE 1953 2085 STLVEVTLGEVYPA 1955 2086 SSTLVEVTLGEVYPA 1955 2086 VELVHFLLLKYRARE 1957 2089 VELVHFLLLKYRARE 1957 2090 VFGIEVVEVPISHL 1959 2090 VFGIEVVEVPISHL 1950 2091 VVPISHLYILVTC 1960 2092 WELSMLEVFGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 VILVTCLGLSYDGLL 1963 2094 VPILVTCLGLSYDGLL 1963 | IMEG | 2069 | LIIVLAIIAÌEGDCA | 1938 | | 0.0120 | | | |
| 2071 LLKYRAREPVTKAEM 1940 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPAADSP 1942 2073 LVEVTLGEVPAADSP 1943 2074 MVELVHFLLLKYRAR 1944 2076 MVELVHFLLLKYRAR 1945 2076 PRKLLMQDLVQENYL 1946 2077 PRMFPDLESEFQAAI 1947 2077 PRMFPDLESEFQAAI 1947 2079 QAAISRKMVELVHFL 1947 2079 QDFPVISKASEYL 1948 2081 QLVFGIEVVEVVPIS 1950 2081 QLVFGIEVVEVVPIS 1951 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1953 2083 REPVTKAEMLESVLR 1953 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILTVTCLGISYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLINLAIAIEG 1956 2090 VFGIEVVEVVPISHL 71LVTC 1958 2091 VVPISHLYILVTCLG 2090 VFGIEVVEVVPISHL 1959 2092 WEELSMLEVFEGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGISYDGLL 1963 2094 YILVTCLGISYDGLL 1963 | IIAIE | 2070 | LLIIVLAIIAIEGDC | 1939 | | 0.0130 | | | |
| 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPAADSP 1942 2074 MVELVHFLLLKYRAR 1943 2075 NQVMFTGLLIVYA 1944 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESEFQAAI 1946 2077 QAAISRKMVELVHFL 1947 2079 QAAISRKMVELVHFL 1947 2081 QLVFGIEVVEVVPIS 1949 QLVFGIEVVEVVPIS 1950 2081 QLVFGIEVVEVVPIS 1951 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVIR 1953 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGISYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLIVLAIAIEG 1955 2087 TGLLIVLAIAIEG 1956 2090 VFGIEVVEVVPISHL 71LVTCLG 2090 VFGIEVVEVVPISHL 11SY 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGISYDGLL 1963 | REPVTK | 2071 | LLKYRAREPVTKAEM | 1940 | | | | | |
| 2073 LVEVTLGEVPAADSP 1942 2074 MVELVHKRAR 1943 2075 NQVMPKTGLLIN'A 1944 2076 PRALLLKYRAR 1945 2077 PRMFPDLESEFQAAI 1945 2078 QAAISRKMVELVHFL 1947 2078 QDFFPVIFSKASEYL 1949 2080 QDFFPVIFSKASEYL 1949 2081 QLVGENVEVPPS 1949 2082 RALIETSYVKVLHHT 1951 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1953 2084 RKLLMQDLVQENYLE 1953 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCGLGSVD 1954 2086 SSTLVRTLGEVPAA 1955 2087 TGLLIN'LAIAIEG 1956 2097 VFGLWYPISHLYILVTC 1959 2099 VVPISHLYILLYYRARE 1956 2090 VFGIEVVEVVPISHL 1959 2090 VVPISHLYILLYTCLG 1960 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 | IEVVEV | 2072 | LQLVFGIEVVEVVPI | 1941 | | | | | |
| 2074 MVELVHFILLKYRAR 1943 2075 NQVMPKTGLLINLA 1945 2076 PRKLLMQDLUQENYL 1945 2077 PRMEDLESEÇAAI 1946 2078 QAAISRKMVELVHFI 1947 2079 QDFPVIFSKASEYL 1948 2080 QDLVQENYLEYRQVP 1949 2081 QLVGENYLEYRQVP 1950 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 2083 REPVTKAEMLESVLR 1953 2084 RKLLMQDLVQENYLE 1953 2085 STLVILVTCGLSVD 1954 2086 STLVILVTCGLSVD 1954 2087 TGLLINLAIAIEG 1955 2087 TGLLINLAIAIEG 1956 2080 VEVPPISHLYILVTC 1959 2090 VFGIEVVEVVPISHL 1959 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCG 1960 2092 WEELSMLEVFGRED 1961 2094 YILVTCLGLSYDGLL 1963 2094 YILVTCLGLSYDGLL 1963 2095 VPFLWGPRALIETSY 1963 | GEVPAA | 2073 | LVEVTLGEVPAADSP | 1942 | | | | | |
| 2075 NQVMPKTGLLIIVIA 1944 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKMVELVHFL 1947 2080 QDLVQENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2082 RALLETSYVKVLHFT 1951 2083 REPVTKAEMLESVLR 1953 2083 REPVTKAEMLESVLR 1953 2084 RKLLMQDLVQENYLE 1953 2085 STLVTLGLSYD 1954 2086 SSTLVETLGEVYAA 1955 2087 TGLLIVTAIAIGG 1956 2088 VELVHFLLLKYRARE 1957 2080 VFGIEVVEVVPISHL 1959 2090 VFGIEVVEVVPISHL 1959 2090 VVPISHLYILVTC 1960 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2094 YILVTCLGLSYDGLL 1965 2094 VILVTCLGLSYDGLL 1965 | FLLLKY | 2074 | MVELVHFLLLKYRAR | 1943 | | | | | |
| 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKMVELVHFL 1947 2079 QDLVGENYLEVRQVP 1949 2081 QLVGENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2082 RALLETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 2083 REPVTKAEMLESVLR 1953 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILTCLGLSVD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLINLAIAIEG 1956 2087 VELVHFLLKYRARE 1957 2089 VELVHFLLKYRARE 1959 2091 VVPISHLYILVTCLG 1958 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 2094 YILVTCLGLSYDGLL 1963 | TGLLII | 2075 | NQVMPKTGLLIIVLA | 1944 | | -0.0011 | | | |
| 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKWELVHFL 1947 2079 QDFPVIFSKASETL 1948 2080 QDLVGENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 2083 REPVTKAEMLESVLR 1953 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGEVPA 1955 2086 SSTLVEVTLGEVPA 1955 2087 TGLLINLAIAIEG 1956 2087 TGLLINLAIAIEG 1956 2087 VELVHFLLKYRARE 1957 2089 VELVHFLLKYRARE 1957 2090 VFGIEVVEVVPISHL 1157 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 | ODLVQE | 2076 | PRKLLMQDLVQENYL | 1945 | | | | | |
| 2078 QAAISRKMVELVHFL 1947 2079 QDFFPVIFSKASEYL 1948 2080 QDLVQENYEVRQVP 1949 2081 QLVGEIVVEVVPIS 1950 2082 RALIETSYVKVLHHT 1951 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2086 SHLYILVTCLGLSVD 1954 2086 STLVTLGEVPA 1955 2087 TGLLINLAIRIEG 1956 2087 TGLLINLAIRIEG 1956 2087 VELVHFLLLKYRARE 1957 2089 VELVHFLLLKYRARE 1957 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YFFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2094 YILVTCLGLSYDGLL 1963 | LESEFQ | 2077 | PRMFPDLESEFQAAI | 1946 | | | | | |
| 2079 QDFFPVIFSKASEYL 1948 2080 QDLVQENYLEYRQVP 1949 2081 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 2083 REPVTKAEMLESVLR 1953 2084 SKILLMQDLVQENYLE 1953 2085 STLVILOTGLSVD 1954 2086 STLVILOTGLSVD 1955 2087 TGLLIVLAIRIEG 1955 2088 VELVHFLLLKYRARE 1957 2089 VEVPPISHLYILYTC 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 2094 VILVTCLGLSYDGLL 1965 | MVELV | 2078 | QAAISRKMVELVHFL | 1947 | | | | | |
| 2080 QDLVQENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2082 RALIETSYVKVLHT 1951 2083 REPYTKAEMIESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2086 SYLLVTCLGLSYD 1954 2086 SYLLVTLGEVRAA 1955 2087 VELVHFLLKYRARE 1955 2087 VELVHFLLKYRARE 1957 2089 VELVHFLLKYRARE 1957 2090 VFGIEVVEVYPISHL 11959 2091 VVPISHLYILVTC 1950 2092 WEELSMLEVFEGRED 1961 2093 YFFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 2095 VFFLWGPRALIETSY 1963 | IFSKAS | 2079 | QDFFPVIFSKASEYL | 1948 | | | | | |
| 2081 QLVFGIEVVEVVPIS 1950 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 4 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGLSYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLINVARIAEG 1956 2088 VELVHFLLKYRARE 1957 2089 VELVHFLLKYRARE 1957 2090 VFGIEVVEVPISHL 11959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1963 2095 VEFLWGPRALIETSY 1963 2095 VEFLWGPRALIETSY 1963 | nyleyr | 2080 | QDLVQENYLEYRQVP | 1949 | | | | | |
| 2082 RALIETSYVKVIJHT 1951 2083 REPYTKAEMLESVIR 1952 2083 REPYTKAEMLESVIR 1952 2084 RKLLMQDLVQENYLE 1953 2085 SHLYIUTCLGLSVD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLINLAIRIEG 1956 2087 TGLLINLAIRIEG 1956 2089 VELVHFILLKYRARE 1957 2090 VFGIEVVEVPISHL 1159 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2094 YILVTCLGLSYDGLL 1963 | :VVEVV | 2081 | QLVFGIEVVEVVPIS | 1950 | | | | | |
| 2083 REPVTKAEMLESVIR 1952 3 2084 RKLLIMQDLVQENYLE 1953 2085 SHLYTUVTCLGLSVD 1954 2086 SSTLVEVTLGEVPA 1955 2087 TGLLINVLAIRIEG 1956 2087 VELVHFILLKYRARE 1957 2089 VELVPISHLYILVTC 1959 2090 VFGISWLYILVTCLG 1960 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2094 VILVTCLGLSYDGLL 1963 | YVKVL | 2082 | RALIETSYVKVLHHT | 1951 | | | | | |
| 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGLSYD 1954 2086 SSTLVBVTLGEVPAA 1955 2087 TGLLINLAIIAIGG 1956 2088 VELVHFLLLKYRARE 1957 2089 VELVPRILLKYRARE 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YFFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2094 VILVTCLGLSYDGLL 1963 2095 VETLWGPRALIETSY 1962 2095 VETLWGPRALIETSY 1963 | AEMLES | 2083 | REPVTKAEMLESVLR | 1952 | | | | | |
| 2085 SHLYILVTCLGLSYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLIIVLAINIEG 1956 2088 VELVHFLLKYRARE 1957 2090 VFGIEVVEVVPISHL YILVTC 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 VFELWGPRALIETSY 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 VPFI WFRA I REGFE- 1963 | DLVQEN | 2084 | RKLLMQDLVQENYLE | 1953 | | | | | |
| 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLINLAIIAEG 1956 2088 VELVHFLLLKYRARE 1957 2089 VEVNPISHLYTIC 1958 2090 VFGIEVVEVVPISHL 2091 VVPISHLYILVTC 1960 2092 WEELSMLEVFERED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 VFFLWGPRALIETSY 1962 2095 VFFLWGFRALIETSY 1962 | TCLGL | 2085 | SHLYILVTCLGLSYD | 1954 | | | | | |
| 2087 TGLLINVLAIRAIEG 2088 VELVHFLLKYRARE 1955 2089 VEVVPISHLYILVTC 1958 2090 VFGIEVVEVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 VPINFRA I REGFE- 1963 | VILGEV | 2086 | SSTLVEVTLGEVPAA | 1955 | | | | | |
| 2088 VELVHFLLKYRARE 2099 VEVVPISHLYILVTC 2090 VFGIEVVEVVPISHL 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGRRALIETSY 2094 YILVTCLGLSYDGLL 2095 VETWGRRALIETSY 2095 VPPI HERA I REGFE. | LAIIA | 2087 | TGLLIIVLAIIAIEG | 1956 | | -0.0011 | | | |
| 2089 VEVVPISHLYILVIC 2090 VFGIEVVEVVPISHL 2091 VVPISHLYILVICLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2005 VPPI HERA I REGEE. | LLLKYR | 2088 | VELVHFLLLKYRARE | 1957 | | | | | |
| 2090 VFGIEVVEVVPISHL 2091 VVPISHL YILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2005 VPPI HERA! REGFE. | HLYIL | 7089 | VEVVPISHLYILVIC | 8661 | | | | | |
| 2091 VVPISHLYILCUG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2005 VPPI HERAT REGFE. | /EVVPI | 2090 | VFGIEVVEVVPISHL | 1959 | | | | | |
| 2092 WEELSMLE VECKED 2093 YETWGPRALIETSY 2094 YILVTCLGLSYDGLL 2095 VPPI HERAT REGEF. | YILVI TENETO | 7007 | VVPISHLYILVICLG | 200 | | | | | |
| 2093 YEFLWGFKALEISY 2094 YILVTCLGLSYDGLL 2004 VEPI HERAI REGEE: | LEVEG | 2027 | WEELSMLEVFECKED | 19 <u>6</u> | | | | - | |
| 2094 TILV ICLUIS I DULL 2005 VPDI HERA I REGEE. | I CALIE | 2007 | YELWGFKALIEIST | 7061 | | | | | |
| | LOLD ID | 2005 | YILVICLOLS I DOLL | 1963 | | | | | |

| | | Tabl | Table XIX A 1 | Mage | 2 DR Sug | er Motif | Mage 2 DR Super Motif Peptides with Binding Data | h Binding | g Data | | | |
|------------------------|-------------------|------------------------------------|------------------------|------------|----------|----------|--|-----------|--------|--------|--------|--------|
| Core Sequence | Core SeqID Num | Exemplary Sequence | Exemplary SeqID Num | Position | DRI | DR2w81 | Position DR1 DR2w81 DR2w282 DR3 DR4w4 DR4w15 DR5w11 DR5w12 | DR3 | DR4w4 | DR4w15 | DR5w11 | DR5w12 |
| VPGSDPACY VLHHTLKIG | 2096 2097 | YROVPGSDPACYEFL YVKVLHHTLKIGGEP | 1965 1966 | 260 285 | | | | | | | i | |

| | | I able AIA A 2 | 4 Z | Mage 2 DR Super | Motif Peptides | Mage 2 DK Super Motil Peptides with Binding Data | | |
|-----------|------------|------------------|-----------|-----------------|----------------|--|-----|-------|
| Core | Core SeqID | Exemplary | Exemplary | DR6w19 | DR7 | DR8w2 | DR9 | DRw53 |
| Sednence | Mun | Sequence | Seq1D Num | | | | | |
| | | | | | | | | |
| VPGSDPACY | 2096 | YRQVPGSDPACYEFL | 1965 | | | | | |
| VLHHTLKIG | 2097 | YVKVLHIHTLKIGGEP | 1966 | | | | | |

| | 5 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|--|------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|--------------------------|-----------------|-----------------|-----------------------------------|-----------------|-----------------|-------------------------|------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|--|-----------------|-----------------|-----------------|-----------------|-----------------|-------------------------------------|-----------------|-----------------|-------------------------|-----------------|------------------------|-----------------|------------------------|-----------------|-----------------|-----------------|------------------------|-----------------|-----------------|-----------------|
| | DR5w12 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | DR5w11 | | | | | | | 0.0310 | | | | | | | | 0000 | 90.0 | | | | | | | -0.0005 | | 0.0650 | 0.00.0 | -0.0005 | | | | | | | | | | | | |
| | DR4w15 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | DR4w4 | 80000 | -0.0032 | -0.0032 | | | | 0.0590 | | | | 0.0110 | | -0.0027 | | 2000 | 0.00 | | -0.008 | | | | -0.0008 | -0.0032 | | -0.0032 | 0.1.0 | 0.0240 | | | | | | | | | | | | |
| ding Data | DR3 | | 0000 | -0.0025 | 0.0058 | | | 0.0059 | | | | | | | | 1 8000 | 200 | | | | | | | 0.0021 | | 9000 | 0,000 | 9000'0 | | 0.0150 | | | | | | | | | | |
| s with Bin | DR2w2B2 | | | | | | | 1.1000 | | | | | | | | 0.000 | 200 | | | | | | | 0.0013 | | 0.0300 | 0.00 | -0.0007 | | | | | | | | | | | | |
| Mage 3 DR Super Motif Peptides with Binding Data | DR2w81 | | | | | | | 0.3100 | | | | | | | | 0.0057 | 0000 | | | | | | | 0.0020 | | 0.0030 | 0.000 | 0.0170 | | | | | | | | | | | | |
| Super M | DRI | 0.0045 | 0.0330 | -0.0003 | | | | 1.9000 | | | | 0.0110 | | 0.0022 | | 0 0003 | 0000 | | 0.0043 | | | | 0.0026 | 0.0250 | | 0.0440 | 3 | 0.0510 | | | | | | | | | | | | |
| Mage 3 DI | Position | 116 | 7 5 | 681 189 | 220 | 272 | 255 | 104 | 49 | 148 | 22 | 175 | 202 203 | 298 | 8 2 | 9/1 | 174 | 134 | 500 | 2 4 5 | 1 23 | 204 | 503 | <u> </u> | 47 | 195 | 76 | 2051 | 30 S | <u>19</u> | 146 | 278 | 7 4 | 115 | 171 | 163 | 142 224 | 271 | 303 | 282 285 |
| IX B 1 | Exemplary SeqID Num | 1961 | 1969 | 1970 | 1972 | 1973 | 1975 | 1976 | 7761 | 1978 | 1980 | 1861 | 1983 | 1984 | 1985 | 1987 | 1988 | 6861 | 0661 | 186 186 186 186 186 186 186 186 186 186 | 1993 | 1994 | 5661 | 1996 | 1998 | 1999 | 2001 | 2002 | 2003 | 2005 | 2006 | 2007 | 5008 2008 | 2010 | 2011 | 2012 | 2013 | 2015 | 2016 | 2018 |
| Table XIX B 1 | Exemplary Sequence | AELVHFLLLKYRARE | ALGLVGAQAPATEEQ | DGLLGDNQIMPKAGL | EEKIWEELSVLEVFE | EFLWGPRALVETSYV | ENYLEYROVPGSDPA | ESEFQAALSRKVAEL | EVTLGEVPAAESPDP | FFFVIFSRASSSLQL FPVIFSRASSSLQL | GEALGLYGAOAPATE | GHLYIFATCLĞLSYD | GLI IIVI.AIIAREGD | GPHISYPPLHEWVLR | HFLLLKYRAREPVTK | HLYIFAICEGESYDG | IGHLYIFATCLGLSY | KAEMLGSVVGNWQYF | KAGLLIIVLAIIARE | KKLLIQHFVQENYLE I GFVPAAFSPDPPOS | LGLVGAQAPATEEQE | LIIVLAIIAREGDCA | LLIIVLAIIAKEGDC | LOLVFGIELMEVDPI | LVEVTLGEVPAAESP | NQIMPKAGLLIIVLA NWOVEFPVIFSK ASS | PSTFPDLESEFOAAL | PVIFSKASSSLQLVF | OAALSKKVAELVHFL | QLVFGIELMEVDPIG | QYFFPVIFSKASSSL | RALVETSYVKVLHHM | SSTI.VEVTI.GEVPAA | VAELVHFLLLKYRAR | VDPIGHLYIFATCLG | VFGIELMEVDPIGHL | WEELSVI.EVFEGRED | YEFLWGPRALVETSY | YPPLHEWVLREGEE- | YVKVLHHMVKISGGP |
| | Core SeqID Num | 2098 | 2100 | 2102 | 2103 | 2104 | 2106 | 2107 | 2108 | 2109 | 2112 | 2112 | 2113 | 2115 | 2116 | 2117 | 2119 | 2120 | 2121 | 2122 | 2124 | 2125 | 2126 | 2128 | 2129 | 2130 | 2132 | 2133 | 2134 | 2136 | 2137 | 2138 | 2139 | 2141 | 2142 | 2143 | 2144 | 2146 | 2147 | 2148 |
| | Core Sequence | VHFLLLKYR | LVGAQAPAT | LSTDGLLGD | IWEELSVLE | WGPRALVET | WEELS VLE V LEYROVPGS | FQAALSRKV | LGEVPAAES | VIFSKASSS | LGLVGAOAP | YIFATCLĞL | LMEVDPIGH IIVI.AIIAR | ISYPPLHEW | LLKYRAREP | MEVIDEGES | LYIFATCLG | MLGSVVGNW | LLIIVLAII | LTQHFVQEN VPAAESPDP | VGAQAPATE | VLAIIAREG | IVLAIIAKE | YKAKEPVIK | VTLGEVPAA | MPKAGLLII | FPDLESEFO | FSKASSSLQ | LSKKVAELV VOENVI EVR | FGIELMEVD | FPVIFSKAS | VETSYVKVL | VINAEMLGS LVEVTLGEV | LVHFLLLKY | IGHLYTFAT | IELMEVDPI | WOYFFPVIII SVIEVFEG | LWGPRALVE | LHEWVLREG | VLHHMVKIS |

- . -

| Core SeqID Exe Num Seq | | Evennlan, | DR6w19 | 707 | • | | |
|------------------------|--------------------------------------|--------------|---------|---------|---------|-----|-------|
| 4 | Sequence | SeqID Num | | DR/ | DK8W2 | DR9 | DRw53 |
| Ş | AELVHFLLLKYRARE | 1961 | | , e c c | | | |
| <u>ي</u> ړ. | AGLLII VLAIIAKEG ALGLVGAQAPATEEQ | 8961 6961 | | -0.0026 | | | |
| ್ರ | CLGLSY DGLLGDNQI DGLLGDNQIMPKAGL | 1970 1971 | | -0.0011 | | | |
| | EEKIWEELSVLEVFE FFI WGPRALVFTSYV | 1972 | | | | | |
| | EKIWEELSVLEVFEG | 1974 | | | | | |
| | ESEFQAALSRKVAEL | 9261 | 0.0005 | 0.7400 | 0.0430 | | |
| | EVTLGEVPAAESPDP | 1977 | | | | | |
| | FPVIFSKASSSLQLV | 1979 | | | | | |
| | GEALGLYGAQAPATE | 1980 | | \$600.0 | | | |
| | GIELMEVDPIGHLYI | 1981 | | 0.0023 | | | |
| | GLLIIVLAIIAREGD | 1983 | | 9100 | | | |
| | HFLLLKYRAREPVTK | 1985 | | -0.0010 | | | |
| | HLYIFATCLGLSYDG | 9861 | | | | | |
| ٩₽ | ELMEVDPIGHLYIF GHLYIFATCLGLSY | 1987 1988 | 0.0130 | 0.002/ | 0.0130 | | |
| Э | KAEMLGSVVGNWQYF | 6861 | | | | | |
| ਲ = | KAGLLIIVLAIIARE | 0661 | | -0.0011 | | | |
| ıω | GEVPAAESPDPPQS | 1992 | | | | | |
| \preceq | GLVGAQAPATEEQE | 1993 | | | | | |
| ⋝⋸ | LIIVLAIIAREGDCA | 1994 | | -0.0018 | | | |
| ~ | LLKYRAREPVTKAEM | 1996 | | | | | |
| ں ب | QLVFGIELMEVDPI | 1997 | 0.0004 | 0.0970 | -0.0004 | | |
| ય 💆 | LVEVILGEVFAAESF NOIMPKAGLLIIVLA | 1999 | | -0 0011 | | | |
| 2 | NWQYFFPVIFSKASS | 2000 | -0.0003 | 0.0560 | 0.2200 | | |
| 는 i | PSTFPDLESEFQAAL | 2001 | 0,000 | 0000 | 90000 | | |
| <u>-</u> ∀ | OAAI SRKVAEI VHFI | 2002 | 0.0240 | 0.0890 | 0.0038 | | |
| 1 | QHFVQENYLEYRQVP | 2004 | | | | | |
| ! حر | QLVFGIELMEVDPIG | 2005 | | | | | |
| _ • | QYFFPVIFSKASSSL | 2006 | | | | | |
| | REPUTK A FML GSVVG | 2007 2008 | | | | | |
| | SSTLVEVTLGEVPAA | 2003 | | | | | |
| | VAELVHFLLLKYRAR | 2010 | | | | | |
| ு மீ | VDPIGHLYIFATCLG | 201 | | | | | |
| | VGNWQYFFPVIFSKA | 2013 | | | | | |
| | WEELSVLEVFEGRED | 2014 | | | | | |
| | YELWGPKALVEISY VPPI HEWAYI REGEE. | 2015 2016 | | | | | |
| - ~ | YRQVPGSDPACYEFL | 2017 | | | | | |
| _ | YVKVLHHMVKISGGP | 2018 | | | | | |

157 (deleted) (deleted)

DR5w12

| 2 | |
|---|---|
| | 2 |
| Lable XXa A Mage 2 DR 3a Motif Peptides with Binding Data | |

| | | TABEL A D | riage 2 Div 3a Mouli I chines with Dilluling Data | chines with | Dillumg Dat | 4 | | |
|-----------|-------------------|------------------------|---|-------------|-------------|-------|-----|-----|
| Core | Core SeqID Num | Exemplary Sequence | Exemplary SeqID Num | DR6w19 | DR7 | DR8w2 | DR9 | DRw |
| LSYDGLLGD | 2150 | CLGLSYDGLLGDNQV | 2019 | | | | | |
| IWEELSMLE | 2151 | EEKIWEELSMLEVFE | 2020 | | | | | |
| LESEFQAAI | 2152 | FPDLESEFQAAISRK | 2021 | | | | | |
| MFPDLESEF | 2153 | GPRMFPDLESEFQAA | 2022 | | | | | |
| IEGDCAPEE | 2154 | IIAIEGDCAPEEKIŴ | 2023 | | | | | |
| IAIEGDCAP | 2155 | LAIIAIEGDCAPEEK | 2024 | | | | | |
| LVQENYLEY | 2156 | MODLVQENYLEYRQV | 2025 | | | | | |
| FGIEVVEVV | 2157 | OLVFGIEVVEVVPIS | 2026 | | | | | |
| LMQDLVQEN | 2158 | RKLLMQDLVQENYLE | 2027 | | | | | |
| LLGDNQVMP | 2159 | YDGLLGDNQVMPKTG | 2028 | | | | | |
| | | | | | | | | |

| | | DR5w12 | | | | | | | | |
|-------------|---|-----------------------------------|-----------------|-----------------|------------------------|------------------|-----------------|-----------------|-----------------|-----------------|
| | | DR5w11 | | | | -0.0008 | | | | |
| | | DR4w15 | | | | | | | | |
| | | DR4w4 | | | | -0.0055 | | | | |
| | <u>22</u> | DR3 | -0.0025 | 0.0058 | 0.0026 | 1.8000 | -0.0025 | 0.0150 | 0.2800 | 0.0080 |
| | Mage 3 DR 3a Motif Peptides with Binding Data | DR2w282 | | | | -0.0010 | | | | |
| (a B | des with B | DR2w2B1 | | | | 0.0057 | | | | |
| Table XXa B | otif Peptio | DRI | | | | 0.0003 | | | | |
| | DR 3a M | Position | 183 | 220 | 001 | 166 | 208 | 191 | 249 | 188 |
| | Mage 3 | Exemplary SeqID Num | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 |
| | | Core SeqID Exemplary Num Sequence | CLGLSYDGLLGDNOI | EEKIWEELSVLEVFÈ | FPDLESEFQAALSRK | IELMEVDPIGHL YIF | LAIIAREGDCAPEEK | QLVFGIELMEVDPIG | TOHFVQENYLEYRQV | YDGLLGDNQIMPKAG |
| | | Core SeqI Num | 2160 | 2161 | 2162 | 2163 | 2164 | 2165 | 2166 | 2167 |
| | | ટ | GLLGD | LSWLE | FOAAL | PIGHL | GDCAP | MEVD | NYLEY | NQIMP |

| | | DR9 | |
|-------------|---|------------------------|--|
| | | DR8w2 | 0.0130 |
| | ta | DR7 | 0.0027 |
| | Binding Da | DR6w19 | 0.0130 |
| Table XXa B | Peptides with | Exemplary SeqID Num | 2029 2030 2031 2032 2033 2034 2035 |
| Ta | Mage 3 DR 3a Motif Peptides with Binding Data | Exemplary Sequence | CLGLSYDGLLGDNQI EEKIWEELSVLEVFE FPDLESFPQAALSRK IELMEVDPIGHLYIF LAIIAREGDCAPEEK QLVFGIELMEVDPIG TQHFVQENYLEYRQV YDGLLGDNQIMPKAG |
| | | Core SeqID Num | 2160 2161 2163 2163 2164 2165 2165 |
| | | Core Sequence | LSYDGLLGD IWEELSVLE LESEFQAAL MEVDPIGHL IAREGDCAP FGIELMEVD FVOENYLEY LLGDNOIMP |

DRw53

| | | | | Tab | Table XXb A | | | | | | |
|------------|-------------------|-----------------------------------|------------------------------|------------|-------------|---|-----|--------|-------|--------------|--------|
| | | | Mage 2 DR | 3b Motif I | eptides | Mage 2 DR 3b Motif Peptides with Binding Data | ata | | | | |
| Core | Core SeqID Num | Core SeqID Exemplary Num Sequence | Exemplary Position SeqID Num | Position | DR1 | DRI DR2w281 DR2w282 | 282 | DR3 | DR4w4 | DR4w4 DR4w15 | DR5w11 |
| AAISRKMVE | ŀ | EFQAAISRKMVELVH | 2037 | 901 | | | | 0.0039 | | | |
| MPLEQRSQH | 2169 | MPLEQRSQHCKP | 2038 | - | | | | | | | |
| IGGEPHISY | | TLKIGGEPHISYPPL | 2039 | 292 | | | 7 | 0.0025 | | | |
| י חתם גוכל | | VKVI HHTI KIGGEPH | 0700 | 286 | | | | 3000 | | | |

| | Table XXb A Mage 2 DR 3b Motif Peptides with Binding Data |
|--|--|
|--|--|

| Core Sequence | Core SeqID Num | Exemplary Sequence | Exemplary DR6w19 DR7 C | DR6w19 | DR7 | DR8w2 | DR9 | DRw53 |
|--|------------------------------|---|------------------------------|--------|-----|-------|-----|-------|
| AAISRKMVE MPLEQRSQH IGGEPHISY LHHTLKIGG | 2168 2169 2170 2171 | EFQAAISRKMVELVH MPLEQRSQHCKP TLKIGGEPHISYPPL VKVLHHTLKIGGEPH | 2037 2038 2039 2040 | | | | | |

| | | נפט |
|-------------|---|---------------------|
| | ; Data | ממיינמת |
| | ith Binding | השהשת ושה ושת |
| Table XXb B | ptides w | ומט |
| Table | 3b Motif Pe | Docition |
| | Mage 3 DR 3b Motif Peptides with Binding Data | Evernolery Docition |
| | | ralar |

| | | | Mage 3 DR 3b Motif Peptides with Binding Data | 3b Motif P | eptides w | ith Bindin | g Data | | | | | |
|------------------|-------------------|------------------------|--|------------|-----------|------------|---------|--------|---------|--------|---------------|--------|
| Core Sequence | Core SeqID Num | Exemplary Sequence | Exemplary Position DR1 DR2w2B1 DR2w2B2 SeqID Num | Position | DR1 | DR2w2B1 | DR2w2B2 | DR3 | DR4w4 | DR4w15 | DR4w15 DR5w11 | DR5w12 |
| ILGDPKKLL | 2172 | EDSILGDPKKLLTQH | 2041 | 237 | 0.0003 | -0.0006 | -0.0010 | 0.6700 | -0.0055 | | -0.0008 | |
| AALSRKVAE | 2173 | EFQAALSRKVAELVH | 2042 | 901 | | | | 0.0027 | | | | |
| MPLEORSOH | 2174 | MPLEORSOHCKP | 2043 | | | | | | | | | |

| Table XXb B | Mage 3 DR 3b Motif Peptides with Binding Data |
|-------------|---|
|-------------|---|

| | | Mage 3 DR 3b Motif Peptides with Binding Data | otif Peptides | with Bindin | g Data | | | |
|------------------|-------------------|---|------------------------|-------------|---------|--------|-----|-------|
| Core Sequence | Core SeqID Num | Exemplary Sequence | Exemplary SeqID Num | DR6w19 DR7 | DR7 | DR8w2 | DR9 | DRw53 |
| ILGDPKKLL | 2172 | EDSILGDPKKLLTQH | 2041 | 0.0130 | -0.0014 | 0.0029 | | |
| AALSRKVAE | 2173 | EFOAALSRKVAELVH | 2042 | | | | | |
| MPLEORSOH | 2174 | MPLEORSOHCKP | 2043 | | | | | |

Table XXII. A2 supermotif analogs

| Source | AA | Sequence | SEQ ID NO: | A*0201 nM | A*0202 nM | A*0203 nM | A*0206 nM | A*6802 nM | No. A2 Alleles Crossbound |
|---------------|----|-----------|------------------|--------------|--------------|--------------|--------------|--------------|---------------------------------|
| MAGE3.112 | 6 | KVAELVHFL | 2214 | 69 | 29 | 14 | 168 | 17 | 5 |
| MAGE3.112L2 | 6 | KLAELVHFL | 2215 | 20 | 6.0 | 5.9 | 12 | 400 | 5 |
| MAGE3.112M2 | 6 | KMAELVHFL | 2216 | 24 | 6.7 | 7.7 | 56 | 286 | 5 |
| MAGE3.112L2V9 | 6 | KLAELVHFV | 2217 | 14 | 13 | 22 | 15 | 73 | S |
| MAGE3.112M2V9 | 6 | KMAELVHFV | 2218 | 26 | 17 | 46 | 39 | 170 | 5 |
| MAGE3.220 | 6 | KIWEELSVL | 2219 | 333 | 391 | 2381 | 308 | : | 3 |
| MAGE3.220L2V9 | 6 | KLWEELSVV | 2220 | 11 | 165 | 20 | 15 | ŀ | 4 |

- indicates binding affinity =10,000nM.

Table XXIIA A01 Analog Peptides

| <u>Peptide</u> | AA | <u>Sequence</u> | SEQ ID NO: | <u>Source</u> | <u>A*0101 nM</u> |
|----------------|------|-----------------|------------|---------------|------------------|
| 52.0026 | 8 | ATCLGLSY | 2221 | MAGE3.179 | 227.3 |
| 52.013 | 11 | VVEVVPISHLY | 2222 | MAGE2.166 | 125 |
| 52.0132 | 11 | TMNYPLWSQSY | 2223 | MAGE3.74 | 301.2 |
| 52.0133 | 11 ` | LMEVDPIGHLY | 2224 | MAGE3.166 | 3.3 |
| 57.0003 | 8 | VTDLGLSY | 2225 | MAGE2.179.D3 | 2.7 |
| 57.0029 | 9 | STFSTTINY | 2226 | MAGE2.69.T2 | 490.2 |
| 57.003 | 9 | MTDLVQENY | 2227 | MAGE2.247.T2 | 8.0 |
| 57.0031 | 9 | STLPTTMNY | 2228 | MAGE3.69.T2 | 58.1 |
| 57.0032 | 9 | GTVVGNWQY | 2229 | MAGE3.137.T2 | 36.2 |
| 57.0033 | 9 | ETDPIGHLY | 2230 | MAGE3.168.T2 | 0.7 |
| 57.0034 | 9 | ITGGPHISY | 2231 | MAGE3.293.T2 | 36.2 |
| 57.0119 | 10 | ATSFSTTINY | 2232 | MAGE2.68.T2 | 454.5 |
| 57.012 | 10 | ASDFSTTINY | 2233 | MAGE2.68.D3 | 25 |
| 57.0121 | 10 | LTQDLVQENY | 2234 | MAGE2.246.T2 | 58.1 |
| 57.0122 | 10 | ATSLPTTMNY | 2235 | MAGE3.68.T2 | 208.3 |
| 57.0123 | 10 | ASDLPTTMNY | 2236 | MAGE3.68.D3 | 2.6 |
| 57.0124 | 10 | LTDHFVQENY | 2237 | MAGE3.246.D3 | 2.3 |

Table XXIIB A03 Analog Peptides

| Peptide | ₹ | Seguence | SEQ ID NO: | Source | A*0301 nM | *1101 nM / | A*3101 nM | A*3301 nM | A*6801 nM | |
|---------|----|-----------|------------|----------------|-----------|------------|-----------|-----------|-----------|----|
| 1371.63 | တ | SVFSTTINK | 2238 | MAGE2.69.V2K9 | 20 | 8.2 | 3333.3 | 9666.7 | 5.7 | 3 |
| 1371.64 | တ | SVFSTTINR | 2239 | MAGE2.69.V2R9 | 57.9 | 6.3 | 62.1 | 87.9 | 6.7 | |
| 1371.65 | 6 | TVINYTLWR | 2240 | MAGE2.73.V2 | 261.9 | 76.9 | 720 | 432.8 | 14.5 | |
| 1371.66 | တ | TVINYTLWK | 2241 | MAGE2.73.V2K9 | 305.6 | 96.8 | 0006 | -58000 | 61.5 | ო |
| 1371.68 | 6 | LVHFLLLKR | 2242 | MAGE2/3.116.R9 | 440 | 375 | 236.8 | 93.5 | 26.7 | Ŋ |
| 1371.69 | တ | YVFPVIFSK | 2243 | MAGE3.138.V2 | 24.4 | က | 2769.2 | 783.8 | 1.7 | ო |
| 1371.7 | တ | YVFPVIFSR | 2244 | MAGE3.138.V2R9 | 35.5 | 2.6 | 9 | 13.2 | 0.5 | 5 |
| 1371.71 | ω | SVFAHPRR | 2245 | MAGE2.237.R8 | 687.5 | 1538.5 | 620.7 | 580 | 156.9 | _ |
| 1371.72 | 6 | AVIETSYVK | 2246 | MAGE2.277.V2 | 392.9 | 62.5 | 12857.1 | -290000 | 30.8 | က |
| 1371.73 | 6 | AVIETSYVR | 2247 | MAGE2.277.V2R9 | 36666.7 | 171.4 | 128.6 | 1160 | 15.4 | ო |
| 1371.74 | တ | IVYPPLHER | 2248 | MAGE2.299.V2 | 117 | 375 | 94.7 | 32.2 | 13.8 | 2 |
| 1371.75 | o. | IVYPPLHEK | 2249 | MAGE2,299,V2K9 | 42.3 | 103.4 | 857 1 | 2989 7 | 42 1 | C. |

Table XXIIC A24 Analog Peptides

| <u>Peptide</u> | AA | Sequence | SEQ ID NO: | Source | <u>A*2401</u> nM |
|----------------|----|--------------------|------------|-----------------|---------------------|
| 52.0072 | 8 | LWGPRALI | 2250 | MAGE2.272 | 100 |
| 52.0073 | 8 | QYFFPVIF | 2251 | MAGE3.144 | 100 |
| 52.0078 | 8 | SYPPLHEW | 2252 | MAGE3.300 | 285.7 |
| 52.0102 | 10 | SYPPLHEWVL | 2253 | MAGE3.300 | 20.3 |
| 52.0166 | 11 | SFSTTINYTLW | 2254 | MAGE2.70 | 428.6 |
| 52.0167 | 11 | IFSKASEYLQL | 2255 | MAGE2.150 | 126.3 |
| 52.017 | 11 | IFSKASSSLQL | 2256 | MAGE3.150 | 131.9 |
| 52.0172 | 11 | IWEELSVLEVF | 2257 | MAGE3.221 | 461.5 |
| 57.006 | 9 | MYPDLESEF | 2258 | MAGE2.97.Y2 | 52.2 |
| 57.0061 | 9 | KYVELVHFF | 2259 | MAGE2.112.Y2F9 | 7.1 |
| 57.0062 | 9 | IYSKASEYF | 2260 | MAGE2.150.Y2F9 | 14.6 |
| 57.0063 | 9 | EYLQLVFGF | 2261 | MAGE2.156.F9 | 4 |
| 57.0064 | 9 | VYPKTGLLF | 2262 | MAGE2.195.Y2F9 | 5.5 |
| 57.0065 | 9 | TYPDLESEF | 2263 | MAGE3.97.Y2 | 218.2 |
| 57.0066 | 9 | NYQYFFPVF | 2264 | MAGE3.142.Y2F9 | 3.4 |
| 57.0067 | 9 | IYSKASSSF | 2265 | MAGE3.150.Y2F9 | 375 |
| 57.0068 | 9 | IYPKAGLLF | 2266 | MAGE3.195.Y2F9 | 9.2 |
| 57.0084 | 10 | SYSTTINYTF | 2267 | MAGE2.70.Y2F10 | 14.8 |
| 57.0085 | 10 | LYILVTCLGF | 2268 | MAGE2.175.F10 | 17.6 |
| 57.0086 | 10 | VYPKTGLLIF | 2269 | MAGE2.195.Y2F10 | 2.9 |
| 57.0087 | 10 | EYLWGPRALF | 2270 | MAGE2.270.Y2F10 | 10 |
| 57.0088 | 10 | SYVKVLHHTF | 2271 | MAGE2.282.F10 | 34.3 |
| 57.009 | 10 | NYQYFFPVIF | 2272 | MAGE3.142.Y2 | 22.6 |
| 57.0092 | 10 | LYIFATCLGF | 2273 | MAGE3.175.F10 | 10 |
| 57.0093 | 10 | IYPKAGLLIF | 2274 | MAGE3.195.Y2F10 | 1.2 |
| 57.0095 | 10 | SYPPLHEWVF | 2275 | MAGE3.300.F10 | 5.5 |

Table XXIII. Immunogenicity of A2 supermotif peptides

| Source | AA | Sequence | SEQ ID NO: | A*0201 nM | A*0202 nM | A*0203 nM | A*0206 nM | A*6802 nM | No. A2 Alleles Crossbound | CTL Wild-type ¹ | CTL |
|------------------|----|-------------|---------------|--------------|--------------|--------------|--------------|--------------|------------------------------|-------------------------------|------|
| MAGE2.112 | 6 | KMVELVHFL | 2276 | 8.6 | 25 | 17 | 123 | 2353 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 10 | KMVELVHFLL | 2277 | 23 | 39 | 127 | 9.0 | 2667 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 11 | KMVELVHFLLL | 2278 | 5.0 | 45 | 63 | 601 | 7692 | 4 | 1/1 | 0/1 |
| MAGE2.153 | 6 | KASEYLQLV | 2279 | 152 | 911 | 17 | 185 | 4878 | 4 | 2/4 | 0/2 |
| MAGE2.157 | 10 | YLQLVFGIEV | 2280 | 20 | 165 | 345 | 370 | 9302 | 4 | 3/3 | 1/3 |
| MAGE2.160 | 10 | LVFGIEVVEV | 2281 | 357 | 20 | 43 | 28 | 8.0 | S | 4/4 | 0/3 |
| MAGE3.112 | 6 | KVAELVHFL | 2282 | 89 | 29 | 14 | 168 | 11 | 5 | 3/4 | 3/4 |
| MAGE3.112 | 10 | KVAELVHFLL | 2283 | 54 | 36 | 217 | 506 | 11 | 5 | 0/1 | 0/1 |
| MAGE3.159 | 11 | QLVFGIELMEV | 2284 | 7.9 | 74 | 217 | 185 | 267 | 5 | 3/3 | 1/32 |
| MAGE3.160 | 10 | LVFGIELMEV | 2285 | 29 | 20 | 7.7 | 28 | 14 | \$ | 4/4 | 1/42 |
| MAGE3.195 | 11 | IMPKAGLLIIV | 2286 | 20 | 226 | 4 | 9/1 | ۳ ا | 4 | 3/4 | 0/3 |
| MAGE3.220 | 6 | KIWEELSVL | 2287 | 357 | 391 | 2381 | 308 | ; | ы | 3/4 | 0/3 |
| MAGE3.271 | 6 | FLWGPRALV | 2288 | 31 | 43 | 14 | 336 | 40 | ς, | 4/4 | 2/4 |

Indicates the number of donors positive over the total number of donors tested.
 A positive result was seen after the second restim.
 - indicates binding affinity =10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

| | | | • | Kad | Radiolabeled peptide | |
|---------|------------|---------|-----------------------|----------------------------|----------------------|------------|
| Species | Antigen | Allele | Cell line | Source | Sequence | SEQ ID NO: |
| Human | Α1 | A*0101 | Steinlin | Hu. J chain 102-110 | YTAVVPLVY | 2289 |
| | A 2 | A*0201 | γ | HBVc 18-27 F6->Y | FLPSDYFPSV | 2290 |
| | A 2 | A*0202 | P815 (transfected) | HBVc 18-27 F6->Y | FLPSDYFPSV | 2291 |
| | A 2 | A*0203 | FUN | HBVc 18-27 F6->Y | FLPSDYFPSV | 2292 |
| | A 2 | A*0206 | CLA | HBVc 18-27 F6->Y | FLPSDYFPSV | 2293 |
| | A 2 | A*0207 | 721.221 (transfected) | HBVc 18-27 F6->Y | FLPSDYFPSV | 2294 |
| | A3 | | GM3107 | non-natural (A3CON1) | KVFPYALINK | 2295 |
| | A11 | | BVR | non-natural (A3CON1) | KVFPYALINK | 2296 |
| | A24 | A*2402 | KAS116 | non-natural (A24CON1) | AYIDNYNKF | 2297 |
| | A31 | A*3101 | SPACH | non-natural (A3CON1) | KVFPYALINK | 2298 |
| | A33 | A*3301 | LWAGS | non-natural (A3CON1) | KVFPYALINK | 2299 |
| | A28/68 | A*6801 | CIR | HBVc 141-151 T7->Y | STLPETYVVRR | 2300 |
| | A28/68 | A*6802 | AMAI | HBV pol 646-654 C4->A | FTQAGYPAL | 2301 |
| | B7 | B*0702 | GM3107 | A2 sigal seq. 5-13 (L7->Y) | APRTLVYLL | 2302 |
| | B8 | B*0801 | Steinlin | HIVgp 586-593 Y1->F, Q5->Y | FLKDYQLL | 2303 |
| | B27 | B*2705 | LG2 | R 60s | FRYNGLIHR | 2304 |
| | B35 | B*3501 | CIR, BVR | non-natural (B35CON2) | FPFKYAAAF | 2305 |
| | B35 | B*3502 | TISI | non-natural (B35CON2) | FPFKYAAAF | 2306 |
| | B35 | B*3503 | EHM | non-natural (B35CON2) | FPFKYAAAF | 2307 |
| | B44 | B*4403 | PITOUT | EF-1 G6->Y | AEMGKYSFY | 2308 |
| | B51 | | KAS116 | non-natural (B35CON2) | FPFKYAAAF | 2309 |
| | B53 | B*5301 | AMAI | non-natural (B35CON2) | FPFKYAAAF | 2310 |
| | B54 | B*5401 | KT3 | non-natural (B35CON2) | FPFKYAAAF | 2311 |
| | Cw4 | Cw*0401 | CIR | non-natural (C4CON1) | QYDDAVYKL | 2312 |
| | Cw6 | Cw*0602 | 721.221 transfected | non-natural (C6CON1) | YRHDGGNVL | 2313 |
| | Cw7 | Cw*0702 | 721.221 transfected | non-natural (C6CON1) | YRHDGGNVL | 2314 |
| Mouse | مو | | EL4 | Adenovirus E1A P7->Y | SGPSNTYPEI | 2315 |
| | . K | | EL4 | VSV NP 52-59 | RGYVFQGL | 2316 |
| | Dq | | P815 | HIV-IIIB ENV G4->Y | RGPYRAFVTI | 2317 |
| | м | | P815 | non-natural (KdCON1) | KFNPMKTYI | 2318 |
| | T | | | | | |

SEO ID NO: 2330 2331 2332 2333 2334 2335 2336 2337 2338 2342 2343 2345 *<u>УАНААНААНААНАА</u>* **ҮАНААНААНААНАА ҮАНААНААНААНАА ҮАНААНААНААНААНАА ҮАНААНААНААНАА** YNTDGSTDYGILQINSR YLEDARRKKAIYEKKK YLEDARRKKAIYEKKK VVHFFKNIVTPRTPPY EALIHQLKINPYVLS YARFQSQTTLKQKT YAAFAAAKTAAAFA YPKYVKQNTLKLAT YARFQRQTTLKAAA YARFQSQTTLKQKT YARFQSQTTLKQKT **PKYVKQNTLKLAT** YARFOSOTTLKOKI QYIKANSKFIGITE QYIKANSKFIGITE **QYIKANSKFIGITE QYIKANAKFIGITE QYIKANAKFIGITE QYIKANSKFIGITE** QYIKANSKFIGITE NGOIGNDPNRDIL YKTIAFDEEARR Sequence Radiolabeled peptide Lambda repressor 12-26 Lambda repressor 12-26 unknown eluted peptide Tet. tox. 830-843 S->A non-natural (717.01) non-natural (ROIV) non-natural (760.16) non-natural (717.01) non-natural (717.10) non-natural (717.01) non-natural (717.01) non-natural (ROIV) non-natural (ROIV) non-natural (ROIV) non-natural (ROIV) Tet. tox. 830-843 MT 65kD Y3-13 Tet. tox. 830-843 Tet. tox. 830-843 MBP 88-102Y HA Y307-319 HA 307-319 HEL 46-61 Source GM3107 or L416.3 LS102.9 L257.6 L255.1 Herluf DB27.4 CH-12 **BIN 40** Sweig H0301 CH-12 .242.5 Preiss Pitout YAR MAT A20 91.7 7466.1 MAT KT3 OLL LUY Œ A20 PF QA1*0301/DQB1*03(**JRB1***0405 **JRB1***0802 ORB1*1302 DRB5*0101 DRB3*0101 **JRB1***0404 **DRB1***0803 DRB5*0201 DRB4*0101 DRB1*0101 **JRB1*1501** ORB1*1601 ORB1*0301 **JRB1***0401 **JRB1***0402 DRB1*0701 DRB1*0901 DRB1*1101 **DRB1*1201** DR4w15 **JR4w14 JR4w10** DR4w4 DR13 DR53 D03.1 DR12 DR52 DR2 DR2 DR3 DR7 DR8 DR8 DR9 DR11 DR51 DR51 ۱۶ ı۸ Ι¥ IA^k Species Human Mouse

B. Class II binding assays

Table XXVI. Crossbinding data A2 supermotif peptides

| Source | ΑA | Sequence | SEQ D DO: | A*0201 nM | A*0202 nM | A*0203 nM | A*0206 nM | A*6802 nM | No. A2 Alleles Crossbound |
|------------|---|-------------|--------------|--------------|--------------|--------------|--------------|--------------|------------------------------|
| MAGE2.112 | 6 | KMVELVHFL | 2347 | 38 | 15 | 9.1 | 49 | 364 | 5 |
| MAGE2.112 | 10 | KMVELVHFLL | 2348 | 23 | 39 | 127 | 0.6 | 7997 | 4 |
| MAGE2.112 | ======================================= | KMVELVHFLLL | 2349 | 5.0 | 45 | 63 | 109 | 7692 | 4 |
| MAGE2.153 | 6 | KASEYLQLV | 2350 | 152 | 116 | 17 | 185 | 4878 | 4 |
| MAGE2.157 | 10 | YLQLVFGIEV | 2351 | 50 | 165 | 345 | 370 | 9302 | 4 |
| MAGE2.160 | 10 | LVFGIEVVEV | 2352 | 357 | 21 | 44 | 59 | 8.0 | 5 |
| MAGE2.220 | 6 | KIWEELSML | 2353 | 167 | 642 | 175 | 59 | : | 3 |
| MAGE2.271 | 6 | FLWGPRALI | 2354 | 238 | 96 | 137 | 1542 | 95 | 4 |
| MAGE2.277 | 10 | ALIETSYVKV | 2355 | 200 | 729 | 125 | 1947 | 3077 | 2 |
| MAGE2/3.44 | 10 | TLVEVTLGEV | 2356 | <i>L</i> 9 | 39 | 4.3 | 218 | 33 | 5 |
| MAGE3.112 | 6 | KVAELVHFL | 2357 | 89 | 53 | 14 | 168 | 17 | 5 |
| MAGE3.112 | 10 | KVAELVHFLL | 2358 | 54 | 36 | 217 | 506 | 11 | S |
| MAGE3.159 | 11 | QLVFGIELMEV | 2359 | 7.9 | 74 | 217 | 185 | 267 | 5 |
| MAGE3.160 | 10 | LVFGIELMEV | 2360 | 53 | 70 | 7.7 | 59 | 14 | 8 |
| MAGE3.174 | 11 | HLYIFATCLGL | 2361 | 99 | 741 | 692 | ; | 4494 | |
| MAGE3.176 | 6 | YIFATCLGL | 2362 | 185 | 45 | 37 | 1028 | 222 | 4 |
| MAGE3.195 | Ξ | IMPKAGLLIIV | 2363 | 70 | 226 | 15 | 176 | ŧ | . 4 |
| MAGE3.220 | 6 | KIWEELSVL | 2364 | 333 | . 391 | 2381 | 308 | ŧ | 3 |
| MAGE3.271 | 6 | FLWGPRALV | 2365 | 31 | 43 | 14 | 336 | 40 | 'n |
| | | | | | | | | | |

-- indicates binding affinity =10,000nM.

Table XXVII. Immunogenicity of A2 supermotif peptides

| Source | AA | Sequence | SEQ ID NO: | A*0201 nM | A*0202 nM | A*0203 nM | A*0206 nM | A*6802 nM | No. A2 Alleles Crossbound | CTL Wild-type ¹ | CTL |
|-----------|----|-------------|---------------|--------------|--------------|--------------|--------------|--------------|------------------------------|-------------------------------|------|
| MAGE2.112 | 6 | KMVELVHFL | 2366 | 8.6 | 25 | 17 | 123 | 2353 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 10 | KMVELVHFLL | 2367 | 23 | 39 | 127 | 9.0 | 2667 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 11 | KMVELVHFLLL | 2368 | 5.0 | 45 | 63 | 109 | 7692 | 4 | 1/1 | 0/1 |
| MAGE2.153 | 6 | KASEYLQLV | 2369 | 152 | 116 | 17 | 185 | 4878 | 4 | 2/4 | 0/2 |
| MAGE2.157 | 10 | YLQLVFGIEV | 2370 | 20 | 165 | 345 | 370 | 9302 | 4 | 3/3 | 1/3 |
| MAGE2.160 | 10 | LVFGIEVVEV | 2371 | 357 | 20 | 43 | 28 | 8.0 | \$ | 4/4 | 0/3 |
| MAGE3.112 | 6 | KVAELVHFL | 2372 | 89 | 53 | 14 | 168 | 17 | 5 | 3/4 | 3/4 |
| MAGE3.112 | 10 | KVAELVHFLL | 2373 | 54 | 36 | 217 | 206 | 11 | 5 | 0/1 | 0/1 |
| MAGE3.159 | 11 | QLVFGIELMEV | 2374 | 7.9 | 74 | 217 | 185 | 267 | 5 | 3/3 | 1/32 |
| MAGE3.160 | 10 | LVFGIELMEV | 2375 | 29 | 20 | 7.7 | 28 | 14 | 5 | 4/4 | 1/42 |
| MAGE3.195 | 11 | IMPKAGLLIIV | 2376 | 20 | 226 | 14 | 176 | ° - | 4 | 3/4 | 0/3 |
| MAGE3.220 | 6 | KIWEELSVL | 2377 | 357 | 391 | 2381 | 308 | ; | င | 3/4 | 0/3 |
| MAGE3.271 | 6 | FLWGPRALV | 2378 | 31 | 43 | 14 | 336 | 40 | \$ | 4/4 | 2/4 |
| | | | | | | | | | | | |

Indicates the number of donors positive over the total number of donors tested.
 A positive result was seen after the second restim.
 - indicates binding affinity =10,000nM.

Table XXVIII. DR supertype primary binding

| Peptide | DR147 Algo Sum | Sequence | SEQ ID NO: | Source | DR1 nM | DR4w4 nM | DR7 nM | DR147 Cross- binding |
|---------|----------------------|------------------------|---------------|------------|-----------|-------------|-----------|----------------------------|
| 39.0282 | 2 | LGEVPAADSPSPPHS | 2379 | MAGE2.50 | | | | 0 |
| 39.0283 | 3 | ESEFQAAISRKMVEL | 2380 | MAGE2.102 | 4.2 | 281 | 49 | 3 |
| 39.0284 | 2 | GIEVVEVVPISHLYI | 2381 | MAGE2.163 | 595 | 6429 | 278 | 2 |
| 39.0285 | 2 | DGLLGDNQVMPKTGL | 2382 | MAGE2.187 | | | | 0 |
| 39.0286 | 2 | NQVMPKTGLLIIVLA | 2383 | MAGE2.193 | 2632 | | | 0 |
| 39.0287 | 2 | KTGLLIIVLAIIAIE | 2384 | MAGE2.198 | 417 | 1216 | 862 | 2 |
| 39.0288 | 2 | TGLLIIVLAIIAIEG | 2385 | MAGE2.199 | 6250 | | | 0 |
| 39.0291 | 2 | GLLIIVLAIIAIEGD | 2386 | MAGE2.200 | 500 | | | 1 |
| 39.0292 | 3 | LLIIVLAIIAIEGDC | 2387 | MAGE2.201 | 581 | 3750 | 1923 | 1 |
| 39.0293 | 2 | LIIVLAIIAIEGDCA | 2388 | MAGE2.202 | 417 | 8824 | 2083 | 1 |
| 39.0294 | 2 | EPHISYPPLHERALR | 2389 | MAGE2.296 | | | | 0 |
| 39.0295 | 3 | ALGLVGAQAPATEEQ | 2390 | MAGE2/3.22 | 152 | | | 1 |
| 39.0296 | 2 | ESEFQAALSRKVAEL | 2391 | MAGE3.102 | 2.6 | 763 | 34 | 3 |
| 39.0297 | 2 | NWQYFFPVIFSKASS | 2392 | MAGE3.142 | 46 | 409 | 446 | 3 |
| 39.0298 | 3 | PVIFSKASSSLQLVF | 2393 | MAGE3.148 | 98 | 1875 | 281 | 2 |
| 39.0299 | 3 | LQLVFGIELMEVDPI | 2394 | MAGE3.158 | 200 | | 258 | 2 |
| 39.0300 | 3 | GHLYIFATCLGLSYD | 2395 | MAGE3.173 | 455 | 4091 | | 1 |
| 39.0301 | 2 | DGLLGDNQIMPKAGL | 2396 | MAGE3.187 | | | | 0 |
| 39.0302 | 2 | NQIMPKAĞLLIIVLA | 2397 | MAGE3.193 | 114 | | | 1 |
| 39.0303 | 2 | KAGLLIIVLAIIARE | 2398 | MAGE3.198 | 1163 | | | 0 |
| 39.0304 | 2 | AGLLIIVLAIIAREG | 2399 | MAGE3.199 | 1111 | | >9615 | 0 |
| 39.0305 | 3 | LLIIVLAIIAREGDC | 2400 | MAGE3.201 | 1923 | | | 0 |
| 39.0306 | 2 | GPHISYPPLHEWVLR | 2401 | MAGE3.296 | 2273 | | | 0 |

⁻⁻ indicates binding affinity =10,000nM.

Table XXIX. DR supertype crossbinding

| OR 147 Broad Cross- Binding binding (5/8) | 3 7 | 2 3 | 2 2 | 3 6 | 3 6 | 2 4 | 2 2 |
|---|-------------------------|-------------------------|-----------------|-------------------------|-----------------|------------------------|-------------------------|
| DR8w2 Cr nM bin | 1581 | 9055 | : | 1140 | 223 | : | ŀ |
| DR5w1 I | 741 | ; | ł | 645 | 308 | : | : |
| DR6w1 9 nM | 522 | 49 | 2333 | 7000 | 1 | 146 | 8750 |
| DR2w2 β2 nM | 20 | : | ; | 18 | <i>L</i> 99 | : | ŀ |
| DR2w2 β1 nM | 147 | 1978 | 2460 | 53 | 3033 | 535 | 4550 |
| DR7 nM | 49 | 278 | 862 | 34 | 446 | 281 | 258 |
| DR4w4 nM | 281 | 6459 | 1216 | 763 | 409 | 1875 | ŀ |
| DR1 nM | 4.2 | 595 | 417 | 5.6 | 46 | 86 | 200 |
| Source | MAGE2.102 | MAGE2.163 | MAGE2.198 | MAGE3.102 | MAGE3.142 | MAGE3.148 | MAGE3.158 |
| SEQ ID NO: | 2402 | 2403 | 2404 | 2405 | 2406 | 2407 | 2408 |
| Sequence | 19.0283 ESEFQAAISRKMVEL | 39.0284 GIEVVEVVPISHLYI | KTGLLIIVLAIIAIE | 39.0296 ESEFQAALSRKVAEL | NWQYFFPVIFSKASS | PVIFSKASSSLQLVF | 39.0299 LQLVFGIELMEVDPI |
| Peptide | 39.0283 | 39.0284 | 39.0287 | 39.0296 | 39.0297 | 39.0298 | 39.0299 |

-- indicates binding affinity =10,000nM.

180

Table XXX. DR3 binding

| Peptide | Sequence | SEQ ID NO: | Source | DR3 nM |
|---------|------------------------|---------------|-----------|-----------|
| 39.0384 | GPRMFPDLESEFQAA | 2409 | MAGE2.94 | 3371 |
| 39.0387 | FPDLESEFQAAISRK | 2410 | MAGE2.98 | |
| 39.0388 | EFQAAISRKMVELVH | 2411 | MAGE2.104 | |
| 39.0389 | QLVFGIEVVEVVPIS | 2412 | MAGE2.159 | |
| 39.0390 | CLGLSYDGLLGDNQV | 2413 | MAGE2.181 | 2143 |
| 39.0391 | YDGLLGDNQVMPKTG | 2414 | MAGE2.186 | |
| 39.0392 | LAIIAIEGDCAPEEK | 2415 | MAGE2.206 | |
| 39.0393 | IIAIEGDCAPEEKIW | 2416 | MAGE2.208 | 4546 |
| 39.0394 | EEKIWEELSMLEVFE | 2417 | MAGE2.218 | |
| 39.0395 | RKLLMQDLVQENYLE | 2418 | MAGE2.243 | 2000 |
| 39.0396 | MQDLVQENYLEYRQV | 2419 | MAGE2.247 | 1500 |
| 39.0397 | VKVLHHTLKIGGEPH | 2420 | MAGE2.284 | |
| 39.0398 | TLKIGGEPHISYPPL | 2421 | MAGE2.290 | |
| 39.0399 | FPDLESEFQAALSRK | 2422 | MAGE3.98 | |
| 39.0400 | EFQAALSRKVAELVH | 2423 | MAGE3.104 | |
| 39.0401 | QLVFGIELMEVDPIG | 2424 | MAGE3.159 | |
| 39.0402 | IELMEVDPIGHLYIF | 2425 | MAGE3.164 | 167 |
| 39.0403 | CLGLSYDGLLGDNQI | 2426 | MAGE3.181 | |
| 39.0404 | YDGLLGDNQIMPKAG | 2427 | MAGE3.186 | |
| 39.0405 | LAIIAREGDCAPEEK | 2428 | MAGE3.206 | |
| 39.0406 | EEKIWEELSVLEVFE | 2429 | MAGE3.218 | |
| 39.0407 | EDSILGDPKKLLTQH | 2430 | MAGE3.235 | 448 |
| 39.0408 | TQHFVQENYLEYRQV | 2431 | MAGE3.247 | 1071 |

⁻⁻ indicates binding affinity =10,000nM.

Table XXXI. HTL Candidates

| Broad DR3 Binding Binder (5/8) | 7 0 | 0 9 | 0 9 | 1 1 | 1 1 |
|--------------------------------------|-----------------|-----------------|------------------------|--|-------------------------|
| DR 147 Cross- binding | 3 | 3 | Э | 0 | 0 |
| DR8w2 nM | 1581 | 1140 | 223 | 3769 | ŀ |
| DR5w1 1 nM | 741 | 645 | 308 | : | : |
| DR6w1 9 nM | 522 | 7000 | : | 569 | 269 |
| DR2w2 β2 nM | 20 | 18 | L 99 | ŀ | ŀ |
| DR2w2 β1 nM | 147 | 53 | 3033 | 1597 | : |
| DR3 nM | : | ; | : | 167 | 448 |
| DR7 nM | 49 | 34 | 446 | 9259 | ŀ |
| DR4w4 nM | 281 | 763 | 409 | >8182 | >8182 |
| DR1 nM | 4.2 | က | 46 | : | 1 |
| if Source | up MAGE2.102 | up MAGE3.102 | up MAGE3.142 | 3 MAGE3.164 | 3 MAGE3.235 |
| : Motif | DR s | DR s | DR s | DR | DR3 |
| SEQ ID NO: | 2432 | 2433 | 2434 | 2435 | 2436 |
| Sequence | ESEFQAAISRKMVEL | ESEFQAALSRKVAEL | NWQYFFPVIFSKASS | 39.0402 IELMEVDPIGHLYIF 2435 DR3 MAGE3.164 | 39.0407 EDSILGDPKKLLTQH |
| Peptide | 39.0283 | 39.0296 | 39.0297 | 39.0402 | 39.0407 |

-- indicates binding affinity =10,000nM.

Table IV. HLA Class I Standard Peptide Binding Affinity.

| ALLELE | STANDARD | SEQUENCE | SEQ ID NO: | STANDARD |
|--------|----------|-------------|------------|---------------|
| | PEPTIDE | | | BINDING |
| | | | | AFFINITY (nM) |
| A*0101 | 944.02 | YLEPAIAKY | 2175 | 25 |
| A*0201 | 941.01 | FLPSDYFPSV | 2176 | 5.0 |
| A*0202 | 941.01 | FLPSDYFPSV | . 2177 | 4.3 |
| A*0203 | 941.01 | FLPSDYFPSV | 2178 | 10 |
| A*0205 | 941.01 | FLPSDYFPSV | 2179 | 4.3 |
| A*0206 | 941.01 | FLPSDYFPSV | 2180 | 3.7 |
| A*0207 | 941.01 | FLPSDYFPSV | 2181 | 23 |
| A*6802 | 1072.34 | YVIKVSARV | 2182 | 8.0 |
| A*0301 | 941.12 | KVFPYALINK | 2183 | 11 |
| A*1101 | 940.06 | AVDLYHFLK | 2184 | 6.0 |
| A*3101 | 941.12 | KVFPYALINK | 2185 | 18 |
| A*3301 | 1083.02 | STLPETYVVRR | 2186 | 29 |
| A*6801 | 941.12 | KVFPYALINK | 2187 | 8.0 |
| A*2402 | 979.02 | AYIDNYNKF | 2188 | 12 |
| B*0702 | 1075.23 | APRTLVYLL | 2189 | 5.5 |
| B*3501 | 1021.05 | FPFKYAAAF | 2190 | 7.2 |
| B51 | 1021.05 | FPFKYAAAF | 2191 | 5.5 |
| B*5301 | 1021.05 | FPFKYAAAF | 2192 | 9.3 |
| B*5401 | 1021.05 | FPFKYAAAF | 2193 | 10 |

Table V. HLA Class II Standard Peptide Binding Affinity.

| Allele | Nomenclature | Standard | Sequence | SEQ ID | Binding |
|-----------|--------------|----------|------------------|--------|----------|
| | | Peptide | | NO: # | Affinity |
| | | | | | (nM) |
| DRB1*0101 | DR1 | 515.01 | PKYVKQNTLKLAT | 2194 | 5.0 |
| DRB1*0301 | DR3 | 829.02 | YKTIAFDEEARR | 2195 | 300 |
| DRB1*0401 | DR4w4 | 515.01 | PKYVKQNTLKLAT | 2196 | 45 |
| DRB1*0404 | DR4w14 | 717.01 | YARFQSQTTLKQKT | 2197 | 50 |
| DRB1*0405 | DR4w15 | 717.01 | YARFQSQTTLKQKT | 2198 | 38 |
| DRB1*0701 | DR7 | 553.01 | QYIKANSKFIGITE | 2199 | 25 |
| DRB1*0802 | DR8w2 | 553.01 | QYIKANSKFIGITE | 2200 | 49 |
| DRB1*0803 | DR8w3 | 553.01 | QYIKANSKFIGITE | 2201 | 1600 |
| DRB1*0901 | DR9 | 553.01 | QYIKANSKFIGITE | 2202 | 75 |
| DRB1*1101 | DR5w11 | 553.01 | QYIKANSKFIGITE | 2203 | 20 |
| DRB1*1201 | DR5w12 | 1200.05 | EALIHQLKINPYVLS | 2204 | 298 |
| DRB1*1302 | DR6w19 | 650.22 | QYIKANAKFIGITE | 2205 | 3.5 |
| DRB1*1501 | DR2w2β1 | 507.02 | GRTQDENPVVHFFKNI | 2206 | 9.1 |
| | | | VTPRTPPP | } | |
| DRB3*0101 | DR52a | 511 | NGQIGNDPNRDIL | 2207 | 470 |
| DRB4*0101 | DRw53 | 717.01 | YARFQSQTTLKQKT | 2208 | 58 |
| DRB5*0101 | DR2w2β2 | 553.01 | QYIKANSKFIGITE | 2209 | 20 |

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table VII.A Mage 2, A01 Supermotif Peptides with Binding Data

| | | | | | · |
|-----------------------|---|---|---|---|---|
| SEQ ID NO. | - 0 W 4 W | | 73221822 | 3 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 33 34 37 37 |
| A*0101 | 0.1700 | 0.0028 | 0.0450 | 0.0430 | 0.2000 |
| No. of Amino Acids | 6 01 01 8 01 | 0==606=60=0 | ∞ <u>-</u> 2 6 6 6 2 5 | 2200002∞0∞ | 6 ∞ I ∞ I |
| Position | 154 68 249 224 115 | 137 137 168 263 263 63 63 107 292 | 245 246 246 116 178 178 148 | 96 69 72 138 138 73 73 149 | 139 179 166 169 176 |
| Sequence | ASEYLOLVF ASSFSTTINY DLVOENYLEY ELSMLEVF ELVHFLLLKY | ESYLRNCQDF ESYLRNCQDF EVFERDSVF EVPESHLY FSTTINYTLW GSDFACYFF GSDFACYFFLW HSPQGASSF ILVTCLGLSY ISRKMVELVHF KIGGEPHISY | KMVELVHF LLMQDLVQENY LLMQDLVQENY LVHFLLLKY LVGENYLEY LVTCLGLSY PVIFSKASEY | RMFPDLESEF SSFSTTINY STTINYTLW SYLRNCQDF SVLRNCQDF TTINYTLW VIFSKASEY | VLRNCQDFF VTCLGLSY VVEVVPISHLY VVPISHLY YILVTCLGLSY |

Table VII B
Mage 3 A01 Supermotif Peptides with Binding Data

| Sequence | Position | No. of Amino Acids | A*0101 | SEQ ID NO. |
|--|---|-----------------------|---------|---|
| ASSLPTTMNY ASSSLQLVF ATCLGLSY | 68 154 179 | <u>0</u> 0 0 | 2.6000 | 38 39 |
| ELSVLEVF ELVHFLLLKY EMI GSVVGNIV | 22. 11.5 12.4 | o ∞ 0 ° | | 2 4 4 5 |
| ENDSTANDANDE EVDPIGHLY EVDPIGHLY | 154 168 168 | 2 o = | 18.0000 | 4 4 4 4 5 4 4 5 4 5 4 5 4 5 4 5 4 5 4 5 |
| FVQENYLEY GSDPACYEF GSDPACYEFI W | 250 263 263 | o o : | | 8 4 4 |
| GSVVGNWQYF GSVVGNWQYF GSVVGNWQYF | 137 137 137 | <u> </u> | 0.0500 | 84 49 80 50 50 5 |
| HISYPPLHEW ISGGPHISY | 298 293 | 01 | 0.0370 | 222 |
| ISYPPLHEW KISGGPHISY KVAELVHF | 299 292 112 | o O ∞ | 0.0011 | 55 55 56 |
| LLTQHFVQENY LMEVDPIGHLY SPRVAEI VHE | 245 166 100 | === | 7.5000 | 28 22 |
| LYHELLIKY | 246 | 20.6 | 0.2600 | 60 61 61 |
| MLGSVVGNW MLGSVVGNWQY PIGHLYIF | 35 35 71 | o <u>=</u> ∞ | | 6 63 2 |
| PSTFPDLESEF PTTMNYPLW QVPGSDPACY SLPTTMNY | 95 72 260 70 | . 6 2 ∞ | | 65 67 88 |
| SLPTTMNYPLW SSLQLYF SSSLQLYF | 5 69 7 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | ∷ | 0.0550 | 69 0 1 7 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 |
| SVVGNWQY SVVGNWQYF SVVGNWQYFF TMNYPLW TTMNYPLW VVGNWQYF | 138 138 74 73 . | 2∞62=∞∞ | 0.0830 | 73 75 76 77 78 |
| VVGNWQYFF YIFATCLGLSY | 139 176 | 6 11 | | 79 80 |

| | Binding Data |
|--------------|--------------------------------|
| Table VIII A | Mage 2 A02 Supermotif with Bin |
| | Mage 2 |

| Sequence | Position | No. of Amino Acids | A*0201 | A*0202 | A*0203 | A*0206 | A*6802 | SEQ ID NO. |
|----------------------------|------------|--|--------|--------|--------|--------|--------|------------|
| | | color of the color | | | | | | |
| AAISRKMV | 107 | ∞ ⊆ | | | | | | <u>8</u> |
| AAISRKMVEL AAISRKMVEI V | 107 | 2 = | | | | | | 78 |
| AllAlEGDCA | 207 | : = | | | | | | S 8 |
| AISRKMVEL | 80 | : 6 | | | | | | . & |
| AISRKMVELV | 80 | . 2 | | | | | | 2 % |
| ALGLYGAOA | 22 | 6 | | | | | | 87 |
| ALGLVGAOAPA | 23 | = | | | | | | · 60 |
| ALIETSYV | 277 | ∞ | | | | | | £ & |
| ALIETSYVKV | 277 | . 0 | | | | | | 8 8 |
| ALIETSYVKVL | 27.7 | = | | | | | | 6 |
| AQAPATEEQQT | 28 | = | | | | | | 92 |
| ATEEQOTA | 32 | œ | | | | | | - 66 |
| CAPEKIWEEL | 215 | = | | | | | | 94 |
| CLGLSYDGL | 181 | 6 | | | | | | 95 |
| CLGLSYDGLL | 181 | 0 | | | | | | 96 |
| CQDFFPVI | 143 | ∞ | | | | | | 26 |
| DLESEFQA | <u>8</u> | ∞ | | | | | | 86 |
| DLESEFQAA | 001 | 6 | | | | | | 66 |
| DLESEFQAAI | 91 | 0 | | | | | | 001 |
| DLVQENYL | 249 | ∞ | | | | | | 101 |
| EALGLVGA | 21 | ∞ | | | | | | 102 |
| EALGLVGAQA | 21 | 0 | | | | | | 103 |
| EARGEALGL | 17 | σ.; | | | | | | <u> </u> |
| EARGEALGLV | 11 | 2 • | | | | | | 501 |
| ELVHFLLL | <u> </u> | ∞ <u> </u> | | | | | | 90 9 |
| FOOTASSST | ς Σ | 2 = | | | | | | /01 |
| FTSYVKVI | 8 80 | - ∝ | | | | | | 8 2 |
| ETSYVKVLHHT | 280 | = | | | | | | <u> </u> |
| EVFEGREDSV | 229 | 2 | | | | | | Ξ |
| EVTLGEVPA | 47 | 6 | | | | | | 112 |
| EVTLGEVPAA | 47 | 0 | | | | | | 113 |
| EVVEVVPI | 165 | ∞ : | | | | | | 114 |
| EVVEVVPISHL | 165 | = | - | | | | | 115 |
| EVVPISHL | 168 | ∞ ; | | | | | | 911 |
| EVVPISHLYI | 891 | 2 | | | | | | 117 |
| EVVPISHLYIL | 891 | = - | | | | | | 81 |
| FAHPRKLL | 239 | ∞ | | | | | | 611 |
| FAHPRKLLM | 239 | ο (| | | | | | 120 |
| FLLLKYRA | 119 | * | | | | | | 121 |
| FLWGPRAL | 271 | ∞ (| | | | | | 122 |
| FLWGPRALI | 271 | ο: | | | | | | 123 |
| FLWGPKALIEI | 1/7 | <u> </u> | | | | | | 124 |
| FOAAISRKMV | 105 | , 01 | | | | | | 126 |

linsh

SEQ ID NO. A*6802 A*0206 Mage 2 A02 Supermotif with Binding Data No. of Amino Acids Position GASSFSTT GASSFSTT GASSFSTT GLEARGEALGL GLEGDNQV GLLGDNQV GLLGDNQV GLLGDNQV GLLGDNQV GLLINLAII GLLINLAII GLLINLAII GLUNLAII GLUNCAII GLVGAQAPA HLYILVTCLGL HLYLVTCLGL HLYLVTCLGL HLYLVTCLGL HLYLVTCLGL HLYLVTCLGL HLYLVTCLGL HLYLVTCLGL HLYLVTCLGL HLYLVTCLGL KAEGDCA IIVLAIIA IIVLAIIA IIVLAIIA IIVLAIIA IIVLAIIA IIVLAIIA IIVLAIIA IIVLAIIA IIVLAIIA KAEGLSNL KAEMLESVL KAELLIIVL KTGLLIIVLA KTGLLIIVLA KTGLLIIVLA KTGLLIIVLA KTGLLIIVLA KTGLLIIVLA KTGLLIIVLA KTGLLIIVLA LAIIAIGGCA LIETSVYKV LIETSVYKV Table VIII A
Mage 2 A02 Supermotif with Binding Data

| | _ | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----------------------|-------|---------|--------|-----------|-------|------------|-----------|----------|------------|-----------|-------------|---------------------|--------------------|-----------|-----------|--------|------------|---------|-----|---------|----------|----------|--------|---------|----------|---------|---------|----------|-----------|--------|---------|----------|--------|---------|---------|----------|-----------|----------|---------------|-----------|--------|---------|-----------|----------|
| SEQ ID NO. | 173 | 175 | 176 | 177 | 178 | 179 | <u>2</u> | <u>.</u> | 182 | 183 | 184 | 185 | 98 | 187 | 88 | 68 | 2 3 | 5 5 | 761 | 561 | 96 | 261 | 197 | 198 | 8 | 200 | 201 | 202 | 203 | 204 | 205 | 506 | 207 | 208 | . 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 |
| A*6802 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| A*0206 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| A*0203 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| A*0202 | | | | | | | | | | | | | | | | | | | | | | | | | • | | | | | | | | | | | | | | | | | | | |
| A*0201 | | | | | | | | | | | | • | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| No. of Amino Acids | 8 6 | . 2 | ∞ : | Ξ, | × c | ъ <u>-</u> | 2 = | _ | 2: | = : | = : | = < | > ⊆ | 2 o | ` = | _ ∝ | o <u>C</u> | 2 = | - • | 0 0 | `= | 2 | . ∞ | 6 | 01 | 6 | 6 | 0 | = | ∞ | 6 | ∞ - | 6 | 01 | 6 | 0 | = | = | ∞ | <u>.</u> | ∞ | 6 | = | 9 |
| Position | 202 | 202 | 186 | 189 | - F | 701 | 100 | 107 | 7 2 | 17: | 07. | 047 | 8 2 | 0°24 | 45 | 6 9 | 99. | 9 9 | 8 % | 2 × | 3 = | 247 | 113 | 113 | 113 | 68 | 193 | 193 | 193 | 31 | 31 | <u>[</u> | 171 | 171 | 65 | \$9 | 65 | 148 | 129 | 129 | 901 | 901 | 90 | 59 |
| Sequence | VLAII | VLAIIAI | CDNOVM | GDNQVMPKT | IVLAI | IVEAU | IVI Aliai | | N I KAKETV | KTKAKEPVI | ODI MORNING | COLVCENTL VEGIEV | LVFGIEV VEGIEVA | EVENIEV V | FVTIGEVPA | FOIEVV | GIEVVEV | FOILVEV | | GACAPAT | HELLKYRA | DLVOENYL | ELVHFL | ELVHFLL | ELVHFLLL | EEEGPRM | VMPKTGL | VMPKTGLL | VMPKTGLLI | TEEQQT | TEEQQTA | HLYIL | HLYILV | HLYILVT | GASSFST | GASSFSTT | GASSFSTTI | FSKASEYL | TKAEML | TKAEMLESV | AISRKM | AISRKMV | AISRKMVEL | PATEEQQT |

| | A.S. | Table VIII A | lage 2 A02 Supermotif with Binding Data |
|--|------|--------------|---|
| | | | Mage |

| SEQ ID NO. | 25222222222222222222222222222222222222 |
|-----------------------|--|
| A*6802 | |
| A*0206 | |
| A*0203 | |
| A*0202 | |
| A*0201 | |
| No. of Amino Acids | |
| Position | 29 159 159 159 179 179 179 188 188 189 189 189 189 189 189 189 18 |
| Sequence | QAPATEEQQTA QLVFGIEVV QLVFGIEVV QLVFGIEVVE QLVFGIEVVE QQTASSSST QQTASSSSTL QVMPKTGLL QVMPKTGLL QVMPKTGLL QVMPKTGLL QVMPKTGLL QVMPKTGLL QVMPKTGLL QVMPKTGLL SVAREPVTKA RAREPVTKA STLVEVTL SVEAHPRKLL SVEAHPRKLL SVEAHPRKLL SVEAHPRKLL SVEAHPRKLL VEVTLGEV VLHTLKI VLH |

| · | SEQ ID NO. | 265 266 266 267 269 270 271 273 |
|--|-----------------------|--|
| | A*6802 | |
| | A*0206 | |
| A with Binding Date | A*0203 | |
| Table VIII A Mage 2 A02 Supermotif with Binding Data | A*0202 | |
| Mage 2 | A*0201 | |
| | No. of Amino Acids | 2621682186 |
| | Position | 166 169 169 176 157 157 283 283 |
| | Sequence | EVVPISHL PISHLYI PISHLYIL PISHLYILV VTCLGL QLVFGI QLVFGIEV KVLHHTT KVLHHTL |

| į | NE | : | le l | with Binding Data |
|---|----|---|--------------|---|
| | C | | Table VIII B | Mage 3 A02 Supermotif with Binding Data |

| Sequence | Position | No. of Amino Acids | A*0201 | A*0202 | A*0203 | A*0206 | A*6802 | SEQ ID NO. |
|--------------------------|----------------|-----------------------|---------|--------|--------|--------|--------|------------|
| AALSRKVA AAI SRKVAEI | 107 | & C | 0 0007 | | | | | 276 |
| AALSRKVAELV | 107 | ? = (| | | | | | 278 |
| AASSSSTL AASSSSTLV | ∞ œ m m | ∞ o^ | 0.0001 | | | | | 279 280 |
| AASSSTLVEV | 38 | =: | | | | | | 281 |
| AIIAREGDCA | 207 | 2 6 | 0.0002 | | | | | 282 |
| ALGLVGAQA ALGLVGAQAPA | 7 27 | ^ = | 0.00.0 | | | | | 284 |
| ALSRKVAEL | 801 | 6 | 0.0050 | | | | | 285 |
| ALSRKVAELV | 108 | 2 ∝ | 0.0001 | | | | | 286 |
| ALVETSYVKV | 27.7 | 01 | 0.0024 | | | | | 288 |
| ALVETSYVKVL | 777 | =: | | | | | | 289 |
| AQAPATEEQEA | 28 | = = | | | | | | 290 291 |
| ATEROFA | 32 | _ 00 | | | | | | 292 |
| CAPEEKIWEEL | 215 | · = | | | | | | 293 |
| CLGLSYDGL | 181 | σ; | 0.0004 | | | | | 294 |
| CLGLSYDGLL | | 2 • | 0.0001 | | | | | 295 206 |
| DLESEFOA | <u>8</u> 8 | 0 0 | 0000 | | | | | 297 |
| DLESEFOAAL | 202 | 01 | 0.0001 | | | | | 298 |
| EAASSST | 37 | ∞ | | | | | | 299 |
| EAASSSTL | 37 | σ: | 0.0001 | | | | | 300 |
| EAASSSTLV FALGI VGA | 37 | 2 ≪ | 0.0001 | | | | | |
| EALGLYGAOA | 5 17 | , 2 | 0.0001 | | | | | 303 |
| EARGEALGL | 11 | 6 | 0.0001 | | | | | 304 |
| EARGEALGLV | 17 | <u>o</u> , | 0.0001 | | | | | 305 |
| ELMEVDPI | 165 | ∞ Ξ | 0,000 | | | | | 306 |
| ELVHFLLI. | 511 | _ •c | 0070.0 | | | | | 308 |
| EQEAASSST | 35 | . 9 | | | | | | 309 |
| EQEAASSSSTL | 35 55 | Ξ, | | | | | | 310 |
| EISYVKVL | 780 | × <u>-</u> | | | | | | 116. |
| EVDPICH | 787 | <u> </u> | | | | | | 313 |
| EVDPIGHT VI | 9 9 | , <u>c</u> | 0 0002 | | | | | 314 |
| EVFEGREDSI | 229 | 22: | 0.0001 | | | | | 315 |
| EVFEGREDSIL | 229 | = | • | | | | | 316 |
| EVTLGEVPA | 47 | σ ⊆ | 0.0001 | | | | | 317 |
| EVILUEVRA |) , | 2 ∞ | 0.000.0 | | | | | 319 |
| FLWGPRAL | 271 | · œ | | , | , | ; | , | 320 |
| FLWGPRALV | 271 | σ: | 0.0820 | 0.0500 | 0.9100 | 0.0043 | 1.1000 | 321 |
| FQAALSRKV | 105 | . 6 | | | | | | 323 |

| Table VIII B | lage 3 A02 Supermotif with Binding Data |
|--------------|---|
| | Mage |
| | |

| SEQ ID NO. | 322 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 |
|-----------------------|--|
| A*6802 | 0.1500 |
| A*0206 | 0.0029 |
| A*0203 | 0.1500 |
| A*0202 A*0203 | 0.0140 |
| A*0201 | 0.0001 0.0002 0.0002 0.0003 0.0003 0.0004 0.0001 0.0001 0.0001 0.0002 0.0002 0.0002 0.0002 0.0003 0.0003 0.00140 0.0002 0.0003 0.0003 0.0003 0.0001 |
| No. of Amino Acids | 5~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ |
| Position | 0.00 |
| Sequence | FQAALSRKVA GASSLPTT GASSLPTT GASSLPTT GASSLPTTM GIEARGEA GLEARGEAL GLEARGEALG GLGDNQI GLGDNQI GLGDNQI GLIIVLAII GLIIVLAII GLIIVLAII GLIIVLAII GLUIVAII IAREGDCA IIVLAII ILGDPKKL ILGDPK |

Table VIII B
Mage 3 A02 Supermotif with Binding Data

| | | | AND C SARIA | Mare 2 Ave Supelmon with Diffills Data | Diguilly Data | | | |
|-----------------------------|------------|-----------------------|-------------|--|---------------|--------|--------|-------------|
| Sequence | Position | No. of Amino Acids | A*0201 | A*0202 | A*0203 | A*0206 | A*6802 | SEQ ID NO. |
| LIIVLAII | 202 | 8 | | | | | | 372 |
| LIIVLAIIA | 202 | ο, | 8000.0 | | | | | 373 |
| LLGDNQIM | 681 | ~ ; | | | | | | 374 |
| LLGDNQIMPKA | 687 | =• | | | | | | 375 |
| ברוועראו | 107 | s c | 1000 | | | | | 0/0 |
| | 701 | v 5 | 0.000 | | | | | 379 |
| | 107 | 2 5 | 0.000 | | | | | 070 |
| LLN I KAKEr V | 17. | 2 : | 1000.0 | | | | | 200 |
| LLN T KAKEPVI | 171 | = = | 1000 | | | | | 280 |
| LLLNYKAKErv | 07. | = = | 0.000 | | | | | 185 |
| LMEVOPIGHL | 90 | 2 ∘ | 0.000.0 | | | | | 382 |
| LOLVFGIEL | 861 | ~ : | | | | | | 383 |
| LOLVEGIELM | 28 | 2: | | | | | | 384 |
| LTQHFVQENYL | 246 | = | ; | | | | | 385 |
| LVETSYVKV | 278 | 6 : | 0.0001 | | | | | 386 |
| LVETSYVKVL | 278 | 2 | 0.0002 | | | | | 387 |
| LVEVTLGEV | 45 | 6 | 0.0001 | | | | | 388 |
| LVEVTLGEVPA | 45 | = | | | | | | 389 |
| LVFGIELM | 091 | ∞ | | | | | | 390 |
| LVFGIELMEV | 160 | 0 | 0.1100 | | | | | 391 |
| LVGAOAPA | 52 | ∵ ∞ | | | | | | 392 |
| LVGACAPAT | . \$2 | • | 0.0001 | | | | | 393 |
| LVHFLLKYRA | <u>9</u> | = | | | | | | 394 |
| MVKISGOPHI | 260 | : 9 | 0.0002 | | | | | 395 |
| NOFFEGER | 68 | ? o | | | | | | 396 |
| NOIMPKAGI | 161 | . 0 | | | | | | 101 |
| NOIMPKAGI | 2 2 | , <u>c</u> | | | | | | 398 |
| NOIMPKAGI II | 193 | ? = | | | | | | 300 |
| PATEROFA | 3.5 | : ∝ | | | | | | 400 |
| PATECLEA | | . 0 | 1000 | | | | | 8 6 |
| יאור ובילניאר מוסחו אובי | , <u>.</u> | ^ C | 1000 | | | | | 10, |
| | | ~ | 0.000 | | | | | 707 |
| PIORIC TIPA I | 1/1 | 2 ∘ | 0.000 | | | | | 504 |
| FOGASSLF1 | G 3 | ⊼ ⊊ | | | | | | 404 |
| POGASSEPT I | e : | 2: | | | | | | 402 |
| POGASSLPTIM | S : | = : | | | | | | 909 |
| PQSPQGASSL | 62 | 0 | | | | | | 407 |
| PTTMNYPL | 77 | ∞ . | | | | | | 408 |
| PVIFSKASSSL | 148 | = | | | | | | 409 |
| PVTKAEML | 129 | ∞ | | | | | | 410 |
| PVTKAEMLGSV | 129 | = | | | | | | 411 |
| OAALSRKV | 901 | ∞ | | | | | | 412 |
| ÓAALSRKVA | 901 | 6 | 0.0001 | | | | | 413 |
| ÖAALSRKVAEL | 901 | = | | | | | | 414 |
| OAPATEEOFA | 29 | 0_ | 0.0001 | | | | | 415 |
| DAPATEFOFAA | 20 | := | | | | | | 416 |
| OIMBK AGI | 100 | ; ∝ | | | | | | 417 |
| Olympic AGE | 104 | o | 0 0001 | | | | | 418 |
| CIMPK AGE I I | 7 75 | , 92 | 0000 | | | | | 419 |
| לוויוו וכססדבו | | 2 | | | | | | \ \ : |

| Table V | Mage 3 A02 Supermotif with Binding Data |
|---------|---|
|---------|---|

| | SEQ ID NO. | 420 | 173 | 777 | 423 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 442 | 443 | 444 | 445 | 446 | 447 | 8448 | 644 | 450 | 457 | 453 | 454 | 455 | 457 | 458 |
|---|-----------------------|-------------|------------|--------------|------------------|-----------|-------------|-----------|-------------|-----------|-----------|------------|-------------|------------|----------|------------|-------------|------------|---------------------------|------------|------------|------------|----------|-----------|------------|------------|---------------|-------------|-------------|-----------|-----------|-------------|----------|------------|------------|-------------|
| | A*6802 | | | | | | | | | | | | | | | | | | | | 0 1600 | | | | | | | | | | | | | | | |
| | A*0206 | | | | | | | | | | | | | | | | | | | | 0.0039 | | | | | | | | | | | | | | | |
| With Binding Data | A*0203 | | | | | | | | | | | | | | | | | | | | 1.6000 | | | | | | | | | | | | | | | |
| Mage 3 Auz Supermotii With Binding Data | A*0202 | | | | | | | | | | | | | | | | | | | | 0.0320 | | | | | | | | | | | | | | | |
| Mage | A*0201 | | 0100.0 | 0.0010 | 000 | 0.0001 | | | | | 0.0001 | 0.0002 | | 0.0035 | ; | 0.0049 | | | 07100 | 0.0 | 0.0250 | | | 0.0001 | 0.000 | 0.0001 | | 6000 | 0.0002 | | 0.0045 | | | 0.0180 | 0.0001 | |
| | No. of Amino Acids | = • | • 0 | `= | <u> </u> | 6 | · = | 6 | = | 6 | 6 | 2 : | = | <u>0</u> | ∞ : | 2 | = : | 2 (| ∞ = | _ ~ | 。 으 | 2 | ∞ | 6 | 2 : | ₽, | × : | = \$ | 2 = | _ ∝ | • • | · = | ∞ | ο • | | Ξ |
| | Position | 194 | 6 5 | 65 | 2 0 0 | 276 | 276 | 125 | 125 | 259 | 237 | 237 | 237 | 02 | 157 | 157 | 157 | ۲. | 43 | £ & | 44 | 247 | 113 | 113 | 113 | 149 | 580 | Q : | 0 <u>0</u> | 48 | 84 | 139 | 143 | 176 282 | 283 | 283 |
| | Sequence | QIMPKAGLLII | OLVEGIE! M | OLVEGIE! MEV | OVPGSDPA | RALVETSYV | RALVETSYVKV | RAREPVTKA | RAREPVTKAEM | RQVPGSDPA | SILGDPKKL | SILGDPKKLL | SILGDPKKLLT | SLPTTMNYPL | SLOLVFGI | SLOLVFGIEL | SLQLVFGIELM | SQHCKPEEGL | STLVEVTL STI VEVTI GEV | TI CEVEA A | TLVEVTLGEV | TOHFVOENYL | VAELVHFL | VAELVHFLL | VAELVHFLLL | VIFSKASSSL | VOENING FYBOX | VCENTLETRUV | VINAEMICOSV | VTI GEVPA | VTLGEVPAA | VVGNWOYFFPV | WQYFFPVI | YIFATCLGL | YVKVI HHMV | YVKVLHHMVKI |

| J) | | Rinding D |
|----|-----------|-----------------------------------|
| | Table IXa | e 2 A03 Supermotif with Binding D |
| | | ٠ |

| SEQ ID NO. | 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 |
|-----------------------|--|
| A*6801 | 0.0280 0.0460 0.0490 0.0990 0.0004 0.0220 0.0026 0.0026 0.0044 0.3800 0.0360 |
| A*330I | 0.0003 0.0190 0.0190 0.8100 0.0047 0.0003 3.2000 0.0010 0.0370 |
| A*310i | 0.0006 0.0006 0.0006 0.0084 0.0007 0.0064 0.0064 0.0130 0.0130 0.00250 |
| A*1101 | 0.0007 0.1900 0.0005 0.0005 0.0003 0.0003 0.0003 0.0003 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0002 0.0003 0.0003 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0002 0.0003 0.0003 0.0004 0.0004 0.0003 0.0003 0.0003 0.0004 0.0004 0.0004 0.0003 0.0003 0.0004 0.0003 0. |
| A*0301 | 0,0009 0,0810 0,0047 0,0004 0,0004 0,0002 0,0002 0,0002 0,0003 |
| No. of Amino Acids | |
| Position | 210 249 249 249 236 236 237 237 240 250 250 250 250 250 250 250 250 250 25 |
| Sequence | ALETSYVK DLVĢENYLEYR DSVFAHPR DSVFAHPR DSVFAHPR ELSMLEVFEGR ELVHFLLKYR ELVHFLLKYR ELVHFLLKYR ESFÇAAISR ELLKYRAR ILGDNQVMPK LLGDNQVMPK LLGDNQVMPK LLGDNQVMPK LLENSYVK LLGDNQVMPK LLENSYVK LLENSYVK LLCONQVMPK LLLKYRAR LLENSYVK LLCONQVMPK LLLKYRAR LLENSYVK RAELLKYR LVHFLLLK PACYEFLWGPR PLEQRSQHCK PLHFRLLK RALETSYVK RAREPYTK SSNQEEEGPR |

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| | | Cable IX E |
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| | ISDICAA | 17 A | |
|----------|---|-----------------|------------|
| 4 | Mage 2 A 24 Supermotil Reptides With Binding Data | th Binding Data | |
| Position | No. of Amino Acids | A*2401 | SEQ ID NO. |
| 108 | 6 | | 531 |
| 277 | - | | 532 |
| 181 | . 6 | | 533 |
| 181 | 01 | | 534 |
| 268 | == | 0.0004 | 535 |
| 001 | 10 | | 536 |
| 249 | • | | 537 |
| 249 | 01 | | 238 |
| 270 | 6 | 90000 | 539 |
| 270 | 01 | 0.0097 | 540 |
| 104 | 01 | 0.0002 | 541 |
| 224 | ∞ | | 542 |
| 311 | | | 643 |

| AISKKMVEL | 108 | • | | 150 |
|--------------------------|-----|--------------|--------|-----|
| ALIETSYVKVL | 277 | = | | 532 |
| CLGLSVDGL | 181 | . • | | 533 |
| CIGINADOLI | | ,10 | | 514 |
| CVEELWOODAL | 348 | 2 = | 0.0004 | 434 |
| CIELLWORKE | 007 | = : | 10000 | 767 |
| DLESETQAAI | 39 | 2 | | 536 |
| DLVQENYL | 249 | œ | | 23/ |
| DLVQENYLEY | 249 | 10 | | 238 |
| EFLWGPRAL | 270 | 6 | 0.0006 | 539 |
| FFI WGPRAII | 270 | 10 | 0.0097 | 240 |
| EEO A ICD KM | 104 | 2 5 | 0 0000 | 541 |
| | 700 | ≥ • | | |
| ELSMLEVF | 577 | × | | 247 |
| ELVHFLLL | 115 | ∞ | | 543 |
| ELVHFLLLKY | 115 | 10 | | 544 |
| ETSYVKVI. | 280 | oc | | 545 |
| EVEEGBEDOVE | 279 | · = | | 546 |
| Charles | 371 | | | 273 |
| EVVEVVEI | 601 | ø; | | .40 |
| EVVEVVPISHL | 165 | = | | 248 |
| EVVPISHL | 168 | ∞ | | 549 |
| EVVPISHLY | 168 | 6 | | 220 |
| FVVPISHI VI | 168 | 9 | | 551 |
| CVVDICTI VII | 891 | | | 655 |
| EVVISHLTIL CW OT VECT | 901 | = « | 3 5000 | 777 |
| EYLQLVFGI | 28 | 6 | 3.3000 | 133 |
| FLWGPRAL | 271 | œ | | 554 |
| FLWGPRALI | 271 | 6 | | 555 |
| GIEVVEVVPI | 163 | -0 | | 556 |
| GLEARGEAL | 15 | 6 | | 557 |
| GLEARGEALGL | 15 | | | 558 |
| MAONOUTE | 88 | : 0 | | 559 |
| C1 11/1 A1 | 000 | ` ` | | 960 |
| ייין און | 000 | 01 | | 195 |
| | 007 | 2.6 | | 500 |
| GLSYDGLL | 583 | ∞ (| | 700 |
| HLYILVICL | 1/4 | 5 | | 203 |
| HLYILVTCLGL | 174 | = | | \$6 |
| HTLKIGGEPHI | 289 | = | | 265 |
| IFSKASEY | 150 | ∞ | | 999 |
| IFSKASEYL | 150 | 6 | 0.0230 | 267 |
| IFSKASEYLOL | 150 | = | 0.0950 | 268 |
| INAIIAI | 203 | 6 | | 269 |
| ILVTCLGL | 177 | • | | 570 |
| ILVTCLGLSY | 177 | 10 | | 571 |
| IVIAIIAI | 204 | · • | | 572 |
| IWEELSMI | 221 |) o c | 0.0007 | 573 |
| IWEEL SMI EVE | 221 | · = | 0.0170 | 574 |
| KIGGEPHI | 292 | : ∝ | | 575 |
| KIGGEPHISY | 292 | 01 | | 576 |
| | | 2 | | |

Table X A
Mage 2. A24 Supermotif Peptides with Binding Data

| | SEQ ID NO. | 5.77 |
|-------------------------------------|-----------------------|--|
| Supermoni repudes with Binding Data | A*2401 | 0.0005 0.1200 0.0186 0.0140 0.0140 0.0150 0.0016 |
| Mage 2 A24 Supermoul F | No. of Amino Acids | ∞ o ∞ o o c = o = o c o o o o o o o c o o o o |
| | Position | 220 220 221 221 232 233 233 234 245 255 257 257 258 258 259 250 250 250 250 250 250 250 250 250 250 |
| | edneuce | IWEELSM MYELVHFL MYELVHFL MYELVHFLL TGLLINL TGLLINL TGLLINL TGLLINL TGLLINL INTAIN INTAIN INTAIN WODLVGENY WORALI VILVICL YILVICL Y |

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| | with Binding Da |
| | with |
| 4 | Supermotif Peptides |
| Table X | if Per |
| H | ermot |
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| | Inge 2 A24 |
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| Sequence | Position | No. of Amino Acids | A*2401 | SEQ ID NO. |
|--|--|-----------------------|-----------------------------|---|
| SVFAHPRKL SVFAHPRKLL SVFAHPRKLLM SVFAHPRKLDM | 237 237 237 138 | 6 01 6 | | 623 624 625 625 |
| SYPENTCOPF SYPELHERAL SYVKVLHHTL TLKIGGEPHI TTNYTH W | 138 300 282 290 73 | <u>0</u> | 0.0003 | 627 629 630 630 |
| VEAPPREL VEAPPRELL VEAUPPRELL VEAUPPRELL | 238 238 33 | ∞ ∞ o> ⊆ | 0.0005 | 632 633 633 |
| VEGREDSVF VIFSKASEY VIFSKASEY VIHTLKI VLHTLKI | 230 230 286 286 296 | 2262∞∞ | 0.0004 | 638 637 637 638 639 |
| VARYTGLL VARKTGLLI VARKTGLLI VTCLGLSY VTCLGLSYDGL | 5 | v ∞ o | -0.0004 0.2300 0.0580 | 64 64 64 64 64 64 64 64 |
| VVEVVPISHL VVEVVPISHLY VVPISHLY VVPISHLYI VVPISHLYI VVPISHLYI YLLYTCLGL YLLYTCLGLSY YLLYTCLGLSY YLLYTCLGLSY YLLYTCLGLSY YLYTCLGLSY YVKVLHHTL YVKVLHHTLKI | 166 169 169 176 176 183 183 183 | | | 647 648 649 650 651 653 653 653 656 |

lineh L

| SEQ ID NO. | 657 | 658 659 | 099 | 199 | 662 | 663 | 664 | 993 | 900 | 899 | 699 | 029 | 671 | 672 | 673 | 674 | 675 | 929 | 677 | 670 | 6.80 | 189 | 682 | 683 | 684 | 585 | 989 | 687 | 988 | 689 | 990 | 692 | 663 | 694 | 969 | 969 | 269 | 869 | 700 | 701 |
|-----------------------|-----------|--------------------------|-------------|-----------|------------|-------------|---------------------------|------------|-------------|----------|---------|------------|------------|----------|-------------|----------|-----------|------------|------------|-----------|----------|-----------|------------|-----------|-------------|----------|-----------|----------|------------|----------|-------------|------------|-----------|-------------|-------------|----------|------------|-----------|--------------------|-----------|
| A*2401 | | | | | | 0.0004 | , co | 0.000 | | | | | 0.0017 | | | | | | | | | | | | | | | | | 8000 O- | 1000.0 | | | | | 0.0120 | | 0.0160 | 0.0910 | |
| No. of Amino Acids | 6 | ⊑ ∞ | ·= | 6 | 02 | = : | <u>o</u> . | . . | × = | : oc | • •• | , 01 | 01 | ∞ | | ∞ | σ: | 01: | = : | 2 = | <u> </u> | . 0 | 01 | . 6 | = | ∞ | 6 | φ; | 2 (| × • | 2 ه | 2 0 | ? o | \ <u></u> | = | ∵∞ | 10 | 6 | ⊑ ∞ |) O |
| Position | 108 | 1/7 | 179 | 181 | | 897 | 96 | 0/7 | 165 | 224 | 115 | 115 | 134 | 280 | 280 | . 168 | 897 | 89. | 920 | 229 | 271 | 250 | 163 | 15 | 15 | 188 | | 200 | 183 | 249 | 240 | 298 | 174 | 174 | 289 | 177 | 177 | 150 | 150 23 8 | 238 |
| Sequence | ALSRKVAEL | ALVEISTVK VL ATCLGLSY | ATCLGLSYDGL | CLGLSYDGL | CLGLSYDGLL | CYEFLWOPKAL | DLESEFQAAL EEI WORD AI | | ELMEVDPIGHL | ELSVLEVF | ELVHFLL | ELVHFLLLKY | EMLGSVVGNW | ETSYVKVL | ETSYVKVLHHM | EVDPIGHL | EVDPIGHLY | EVDPIGALYI | EVERGREDSI | EVEGREDSI | FLWGPRAL | FVQENYLEY | GIELMEVDPI | GLEARGEAL | GLEARGEALGL | GLLGDNQI | GLIGUNGIM | GLLIVLAI | ייים אלאטן | HEVOENYI | HEVOENYI EV | HISYPPLHEW | HLYIFATCI | HLYIFATCLGL | HMVKISGGPHI | IFATCLGL | IFATCLGLSY | IFSKASSSL | ILGDPKKL | ILGDPKKLL |

Table X B
Mage 3 A24 Supermotif Peptides with Binding Data

| SEQ ID NO. | 702 705 706 707 708 711 712 713 722 723 724 725 727 727 727 727 727 727 727 727 727 | 2,2 2,2 2,3 3,3 3,3 4,4 4,4 4,5 4,5 4,5 4,5 4,5 4,5 4,5 4,5 |
|-----------------------|--|--|
| Á*2401 | 0.4200 0.0500 -0.0004 0.0260 | 0.0140 0.0480 0.5300 0.0170 0.0270 |
| No. of Amino Acids | & 6 2 % I % 2 6 % 6 2 I 6 % 8 % 6 I 2 I 2 I 2 E 6 | o~2o=2o2o∞o=∞∞o2=∞o5 |
| Position | 195 195 195 221 220 220 221 112 220 231 246 246 246 246 246 246 246 246 246 246 | 55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 |
| Sequence | IMPKAGLL IMPKAGLLI IMPKAGLLII IMPKAGLLII IWEELSVL IWEELSVLEVF KISGGPHI KISGGPHI KISGGPHI KVAELVHF KVAELVHFLL KVAELVHFLL KVAELVHFLL KVAELVHFLL LUINLAII LLINLAII LLINL | LVHFLLLKY LYIFATCL LYIFATCLGL MLGSVYGNW MLGSVYGNWQY MVKISGGPHI NWQYFFPVI NWQYFFPVI NWQYFFPVI NWQYFFPVI NYPLWSQSY PIGHLYIF PTTMNYPLW PYTKAEML QIMPKAGLL QIMPKAGLL QIMPKAGLL QIMPKAGLLI |



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| | Binding Data |
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| aple | otif Pe |
| | Superm |
| | A24 |
| | Mage 3 |

| SEQ ID NO. | 74 74 75 75 75 75 75 76 76 76 76 76 76 76 76 76 76 |
|-----------------------|---|
| A*2401 | 0.1200 0.0026 0.0420 0.0049 -0.0004 -0.0005 |
| No. of Amino Acids | 8608018010886018060186000 860080180180180000000000 |
| Position | 144 237 237 70 70 70 157 157 138 138 138 138 139 139 139 139 139 139 139 139 139 139 |
| Sequence | QYFFPVIF SILGDPKKLL SILGDPKKLL SLETTMNYPL SLPTTMNYPLW SLQLVFGIEL SLQLVFGIEL SLQLVFGIEL SLQLVFGIEL STQLVFGIEL STQLVFGIEL STQLVFGIEL STQLVFGIEL STQLVFGIEL SYVGNWQYF SYVGNWQYF SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW SYPPLHEWW VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI VFGGREDSI SYGNWQYF VVGNWQYF VVGNWQYF VVGNWQYF VVGNWQYF VYGNWQYF |

Table XIA Mage 2. B07 Supermotif Peptides with Binding Data

| PARTEROGYA 30 10 0.0002 APERCONAL 10 0.0002 APERCONAL 265 9 0.0001 DRACYEEL 265 9 0.0001 DRACYEEL 265 9 0.0001 DRACYEEL 266 9 0.0001 DRACYEEL 266 9 0.0001 BHISYPA 266 0.0001 0.0001 PPDLESEPA 98 11 0.0002 PPDLESEPA 98 0.0002 | Sequence | Position | No. of Amino Acids | B*0702 | SEQ ID NO. |
|---|----------|----------|-----------------------|---------|------------|
| 265 265 265 265 265 276 1128 88 99 98 147 147 147 147 147 147 147 147 | ۷. | 30 | 0.5 | 0.0002 | 778 |
| 265 296 296 128 128 128 98 98 98 147 147 147 147 274 274 274 274 274 11 196 196 196 196 197 11 11 11 11 11 11 11 11 11 11 11 11 11 | | 265 | 2 ∞ | -0.0002 | 780 |
| 296 128 128 98 98 98 98 147 147 147 147 147 148 149 149 149 149 149 149 149 149 150 160 160 170 170 180 180 170 180 180 180 180 180 180 180 180 180 18 | -> | 265 | 6 | 0.0001 | 181 |
| 128 98 98 98 147 147 147 147 147 147 148 149 140 140 140 140 140 140 140 140 | | 296 | 6 | 0.1100 | 782 |
| 128 98 98 98 147 147 147 147 274 274 274 274 11 11 11 12 13 19 19 19 19 10 10 10 10 10 10 10 10 10 10 | | 128 | ∞ | 0.0010 | 783 |
| 98 98 98 147 147 147 274 274 274 274 11 196 196 196 196 196 196 196 | ٦ | 128 | 0 | 0.0001 | 784 |
| 98 10 147 147 11 274 274 10 275 274 10 276 274 10 277 274 10 10 10 10 10 10 10 10 10 10 | | 86 | ∞ | -0.0002 | 785 |
| 98 147 147 147 274 274 274 274 274 301 275 377 377 378 378 378 378 378 378 378 378 | × | 86 | 01 | 0.0002 | 786 |
| 147 8 147 11 274 11 94 8 241 11 10 241 11 196 8 196 9 61 11 302 8 60 9 64 8 8 64 8 8 65 6 64 8 8 170 9 170 9 170 170 9 10 | AA(| 86 | = | -0.0001 | 787 |
| . 274 11 274 277 11 274 277 11 241 11 196 8 196 9 196 10 196 11 61 8 60 9 60 9 64 8 8 8 60 9 64 8 170 8 170 9 170 9 170 170 10 | | 147 | ∞ | 0.0003 | 788 |
| 274 10 274 11 94 8 241 10 196 8 196 8 196 9 61 8 61 8 60 9 64 8 8 8 60 9 64 8 8 8 11 1 12 261 11 170 9 170 9 170 170 10 | EY | 147 | = | 0.0004 | 789 |
| 274 11 94 8 241 10 196 8 196 8 196 8 196 11 61 8 61 8 60 9 64 8 8 8 11 11 261 11 261 9 261 9 170 9 170 9 170 9 170 170 10 | <u>}</u> | 274 | 01 | 0.0008 | 190 |
| 241 8 241 10 196 8 196 8 196 10 196 10 197 10 10 10 10 10 10 10 10 10 10 10 10 10 1 | ١,٨٧ | 274 | = | 0.1300 | 162 |
| 241 10 11 8 8 196 8 8 196 9 9 196 10 196 11 302 8 8 60 9 9 64 8 8 58 11 170 8 8 170 9 9 170 9 9 170 9 9 171 11 170 8 8 170 9 9 | | 94 | ∞ | 0.0063 | 792 |
| . 241 11 196 8 196 9 196 10 196 10 196 11 302 8 60 9 64 8 8 8 64 8 8 8 11 170 8 170 9 170 9 10 | JQ. | 241 | 01 | 0.0400 | 793 |
| 11 8 8 196 9 9 196 196 196 196 196 196 196 196 | סרא | . 241 | = | 0.0042 | 794 |
| 196 8 196 | | = | œ | -0.0002 | 795 |
| 196 196 196 196 61 61 8302 84 85 60 60 64 88 261 170 170 170 170 170 170 170 170 170 17 | | 961 | ∞ | 0.0190 | 796 |
| 196 10 196 11 61 8 8 61 11 302 8 8 64 8 8 58 9 64 8 8 58 11 70 9 9 170 8 8 170 9 9 170 8 8 301 8 | | 961 | 6 | 0.0020 | 797 |
| 196 61 8 61 302 8 60 64 8 8 261 170 170 170 170 170 170 170 18 170 170 170 170 170 170 170 170 170 170 | > | 961 | 01 | 0.0003 | 798 |
| 61 8 61 11 302 8 60 9 64 8 58 11 261 9 261 17 170 8 301 8 | ۸۲ | 961 | = | 0.0099 | 462 |
| 61 11 302 8 60 8 64 8 58 8 11 261 9 261 17 170 8 170 9 301 8 | | 61 | 00 | -0.0002 | 800 |
| 302 8 60 9 64 8 58 11 261 9 170 8 170 9 301 8 | SSF | 19 | = | -0.0003 | 801 |
| 60 9 64 8 58 11 261 9 170 8 170 8 301 8 301 8 | | 302 | • | 0.0026 | 802 |
| 64 8 58 11 261 11 170 8 170 9 170 10 301 8 | 4 | 09 | 6 | 0.0001 | 803 |
| 261 11 261 9 261 11 170 8 170 9 301 8 301 8 | | \$ | . ∞ | 0.0007 | 804 |
| 261 9 261 11 170 8 170 9 170 10 301 8 | AD(| 58 | = | 90000 | 805 |
| 261 11 170 8 170 9 170 10 301 8 | .>- | 261 | 6 | 0.0001 | 809 |
| 170 8 170 9 170 10 301 8 301 9 | YEF | 261 | == | -0.0001 | 807 |
| 170 9 170 10 301 8 301 9 | | 170 | ∞ | 0.0170 | 808 |
| 170 10 301 8 301 9 | | 170 | 6 | 0.2500 | 808 |
| 301 8 301 9 | > | 170 | 01 | 0.0027 | 810 |
| 301 9 | | 301 | ∞ | -0.0002 | 811 |
| | _ | 301 | 6 | 0.2700 | 812 |



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| | vith Binding |
| 3 Y | eptides y |
| Table X | B07 Supermotif Peptides |
| | B07 Sup |
| | Mage 3 B(|

| Sequence | Position | No. of Amino Acids | B*0702 | SEQ ID NO. |
|--|--|---|--|---------------------------------------|
| APATEEQEA APATEEQEA APATEEQEAA BPACYEFLW BPACYEFLW BPROSPQGA EPVTKAEML EPVTKAEML EPVTKAEML EPVTKAEML GPRALVETSY GPRALUII MPKAGLLII MPKAGLLII MPKAGLLII MPKAGLLII MPKAGLLII MPKAGLLII MPKAGLLIIVL PPLIEWVL PPLIE | 25.5 25.5 25.5 25.5 25.5 25.5 25.5 25.5 | o 2 2 ∞ o ∞ o 2 2 = o ∞ o ∞ 2 = ∞ o 2 = ∞ o 0 ≈ o 2 = ∞ o = c | 0.0001 0.0002 0.0002 0.0001 0.0001 0.0001 0.0001 0.0001 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0003 | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 |
| YPLWSUSY YPPLHEWV YPPLHEWVL | 301 301 | ∞ ∞ <i>o</i> ⁄ | -0.0002 -0.0002 0.0027 | 848 849 850 |

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| TUNEDITO | Mage 2 B27 Supermotif Peptides |
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| | | Allino Acids | |
|-------------|-----|--------------|-----|
| AHPRKILM | 240 | ~ | 851 |
| AHPRKLLMODL | 240 | · = | 852 |
| REPVTKAEM | 126 | 01 | 853 |
| REPVTKAEML | 126 | = | 854 |
| RGEALGL | 18 | 8 | 855 |
| EKIWEELSM | 219 | 6 | 856 |
| KIWEELSML | 219 | 10 | 857 |
| UGGEPHI | 291 | 6 | 858 |
| KIGGEPHISY | 291 | = | 829 |
| RNCODFF | 140 | 8 | 860 |
| RNCODFFPVI | 140 | = | 198 |
| PHISYPPL | 297 | 80 | 862 |
| HSPOGASSF | 62 | 10 | 863 |
| KTGLLII | 197 | ∞ | 864 |
| KTGLLIIVL | 197 | 10 | 865 |
| RALIETSY | 275 | 6 | 998 |
| PRKLLMQDL | 242 | 6 | 867 |
| RMFPDLESEF | 95 | = | 898 |
| QHCKPEEGL | ∞ | 6 | 698 |
| KLLMQDL | 243 | 88 | 870 |
| RKMVELVHF | Ξ | 6 | 871 |
| KMVELVHFL | Ξ | 0 | 872 |
| RKMVELVHFLL | Ξ | = | 873 |
| HLYILVTCL | 173 | 01 | 874 |
| KASEYLQL | 152 | 6 | 875 |
| KASEYLOLVF | 152 | = | 876 |
| SRKMVELVHF | 110 | 10 | 877 |
| SRKMVELVHFL | 110 | = | 878 |
| KAEMLESVL | 131 | 10 | 879 |
| VHFLLLKY | 117 | 80 | 880 |
| VKVLHHTL | 284 | ∞ | 881 |
| KVLHHTLKI | 284 | 10 | 882 |

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|------|----|----|---|-----------|
| /== | | | | Table XII |

| | Mage 3 B27 Supermotif Peptides | rmotif Peptides | |
|------------|--------------------------------|-----------------------|------------|
| Sequence | Position | No. of Amino Acids | SEQ ID NO. |
| REPUTKAEM | 126 | 01 | 883 |
| REPVTKAEML | 126 | = | 884 |
| RGEALGL | 8 | ∞ | 885 |
| KIWEELSVL | 219 | 01 | 886 |
| HLYIFATCL | 173 | 10 | 887 |
| KLLTOHF | 243 | 80 | 888 |
| HISYPPL | 297 | ∞ | 888 |
| HISYPPLHEW | 297 | = | 068 |
| KAGLLII | 197 | 80 | 168 |
| KAGLLIIVL | 197 | 10 | 892 |
| KKLLTOHF | 242 | 6 | 893 |
| RALVETSY | 275 | 6 | 894 |
| HCKPEEGL | ∞ | 6 | 895 |
| HFVQENY | 248 | ∞ | 968 |
| HFVÖENYL | 248 | 6 | 897 |
| HFVOENYLEY | 248 | = | 868 |
| KVAÈLVHF | Ξ | 6 | 668 |
| KVAELVHFL | Ξ | 01 | 006 |
| KVAELVHFLL | Ξ | = | 106 |
| KASSSLOL | 152 | 6 | 902 |
| KASSSLOLVF | 152 | = | 903 |
| RKVAELVHF | 110 | 10 | 904 |
| RKVAELVHFL | 110 | = | 905 |
| HFLLLKY | 117 | ∞ | 906 |
| KISGGPHI | 291 | 6 | 200 |
| KISGGPHISY | 291 | <u> </u> | 806 |
| KVLHHMVKI | 784 | 2 | 101 |

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Table XIII A Mage 2 B58 Supermotif Reptides Position

Sequence

SEQ ID NO.

| | Ami | Amino Acids | |
|-----------------------|----------|-------------|------------|
| VALICEVALV | 101 | | 010 |
| A A ICDV MAVET | 107 | 9 | 210 |
| A A ICOVIANCE V | 701 | 2 = | - 6 |
| AAISANII VELV | | _ • | ; ; |
| ASETICALY | *** | 0 0 | 2 5 |
| ASETLÇLVF | *C | ~ : | <u>+</u> : |
| ASEYLOLVFG | <u>*</u> | = • | 2:5 |
| ASSESTII | 80 | × | 9 |
| ASSFSTTINY | 89 | 01 | 917 |
| ASSSSTLV | 39 | ∞ | 816 |
| ASSSTLVEV | 39 | 10 | 616 |
| CAPFEKIW | 215 | ; oc | 920 |
| | 310 | | 6 |
| CAFERIWEEL | 21.5 | _ | 17.6 |
| DSVFAHFRKL | 230 | 2: | 77,6 |
| DSVFAHPRKLL | 730 | = . | 576 |
| EARGEALGL | 17 | 6 | 924 |
| EARGEALGLV | 17 | 01 | 925 |
| ESEFOAAI | 102 | ∞ | 926 |
| | 137 | . 2 | 7,00 |
| | 101 | 2 = | 3 8 |
| ESVLKNCQDFF | 13/ | = • | 076 |
| ETSYVKVL | 780 | × × | 67.5 |
| FAHPRKLL | 239 | ∞ | 930 |
| FAHPRKLLM | 239 | 6 | 33 |
| FSKASEYL | 151 | 8 | 932 |
| ECK ASEVI OI | 151 | 01 | 933 |
| SKASEVI DI V | 151 | · - | 020 |
| TONOUT LALLY | | | 360 |
| FSITINYIL | 7 : | × : | 3 3 |
| FSTTINYTLW | 1/ | 2 - | 5 |
| GASSFSTTI | 29 | 6 | 937 |
| GASSFSTTINY | 29 | = | 938 |
| GSDPACYEF | 263 | 6 | 626 |
| GSDPACYEFL | 263 | 01 | 940 |
| GSDPACYEFLW | 263 | = | 94 |
| HSPOGASSF | 63 | 6 | 942 |
| HTI KIGGEPHI | 289 | | 943 |
| VIIV IN | 172 | . 00 | 944 |
| SHI VI VICI | 172 | = | 945 |
| SRKMVFI | 501 | ∵ ∞ | 946 |
| SRKMVELV | 601 | . 6 | 947 |
| ISRKMVEI VHE | 601 | · = | 948 |
| SVPPI HERAL | 299 | _ | 949 |
| KAFMI FCV | 132 | . 00 | 950 |
| K A EMI FCVI | 132 | . 0 | 951 |
| KACEVI OI | 151 | · • | 952 |
| NASCILAL VASEVIOLV | <u> </u> | o 0 | 953 |
| NASETLALV | 163 | \ <u>1</u> | 250 |
| KASETLŲLVF | 501 | 2 ∘ | 500 |
| KiGLLiiV | 198 | • | 7, |

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Table XIII A Mage 2 B58 Supermotif Peptides

| Sequence | Position | No. of Amino Acids | SEQ ID NO. |
|--------------------|----------|-----------------------|------------|
| KTGLLIIVL | 861 | 6 | 926 |
| KTGLLIIVLAI | 861 | = | 156 |
| PACYEFLW | 266 | ∞ | 958 |
| QAAISRKM | 901 | 80 | 656 |
| ÓAAISRKMV | 901 | 6 | 096 |
| QAAISRKMVEL | 106 | = | 196 |
| ÒTASSSSTL | 37 | 6 | 962 |
| OTASSSSTLV | 37 | 01 | 963 |
| RALIETSY | 276 | ∞ | 964 |
| RALIETSYV | 276 | 6 | 965 |
| RALIETSYVKV | 276 | = | 996 |
| RAREPVTKAEM | 125 | = | 196 |
| RSOHCKPEEGL | 9 | = | 896 |
| SSFSTTINY | 69 | 6 | 696 |
| SSFSTTINYTL | 69 | = | 970 |
| SSNQEEEGPRM | . 87 | = | 176 |
| SSSSTLVEV | 40 | 6 | 972 |
| SSSSTLVEVTL | 40 | = | 973 |
| SSSTLVEV | 41 | & | 974 |
| SSSTLVEVTL | 41 | 10 | 975 |
| SSTLVEVTL | 42 | 6 | 926 |
| STLVEVTL | 43 | ∞ | 716 |
| STLVEVTLGEV | 43 | = | 978 |
| STTINYTL | 72 | ∞ | 626 |
| STTINYTLW | 72 | 6 | 086 |
| TASSSSTL | 38 | ∞ | 186 |
| TASSSSTLV | 38 | 6 | 982 |
| TASSSSTLVEV | 38 | = | 983 |
| TSYVKVLHHTL | 281 | Ξ | 984 |
| TTINYTLW | 57 | ∞ 1 | 586 |
| VICLGLSY | 179 | ∞ ∶ | 986 |
| VTCLGLSYDGL | 179 | = : | 787 |
| VIKAEMLESV | 051 | 0 - | 886 |
| VINAEIMLES VE | 95 | - | 186 |

| | 301 | |
|---|-----|--|
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SEQ ID NO.

| Table XIII B Mage 3 BS8 Supermotif Peptides | No. of Amino Acids | 01 | - ∞ | o == | :∞: | 0- • | o 0 | = | ∞ ⊆ | ⊇ ∝ | · = | & | = 5 | 2 - | - 6 | 01 | 6 01 | . ∞ | ∞ = | 5.00 | ∞ . | 1.0 | 6 | 5 | 01 | | 0. | Ξ ο | ν 6 | 10 | ~ ∞ | 6 | • • | = |
|--|-----------------------|------|---------------|------------|-----|------|----------|------|-----|------|------|-----|------|-----|------------|-----|----------|-----|--------------|------|------------|--------------|-----|-----------|------|-------------|------|-------------|-----|------------|-------|-----|----------------|------|
| Table Mage 3 B58 Su | Position | 107 | 388 | 38 88 | 89 | 89 | <u> </u> | 154 | 39 | 95 | 179 | 215 | 215 | 236 | 236 | 37 | 17 | 102 | 280 | 927 | 181 | <u> </u> | 67 | 9/ 263 | 263 | 263 137 | 137 | 137 | 299 | 299 | 132 | 132 | 86! 86! | 861 |
| | | VAEL | יייייי . ר | LV LVEV | Σ | ××× | .VF | VFGI | V . | ^ C. | YDGL | 3 | WEEL | KKL | NNLL TL | TLV | 75 75 | | /L // HHM | SY | <u>.</u> ب | וסר. רסר. | WL. | YEF | YEFL | rer. WOY | WQYF | WQYFF :V | EW. | EWV SWA | SV SV | ^^S | \ \ | /LAI |

| | Table XIII B | 8 4 | |
|-------------|---|--|-----------|
| Sequence | Mage 3 B58 Supermotif Reptides Position A | otil Keptides No. of Amino Acids | SEQ ID NO |
| | | | 7001 |
| KASSSLQL | 133 | ∞ | 001 |
| KASSSLQLV | 55. | ~ \$ | 1037 |
| KASSSLQLVF | 53 | 01 | 1038 |
| LSRKVAEL | 109 | ∞ : | 1039 |
| LSRKVAELV | 109 | 6 | 1040 |
| LSRKVAELVHF | 109 | = | 1041 |
| LTOHFVOENY | 246 | 10 | 1042 |
| LTOHEVOENYL | 246 | = | 1043 |
| PACYEFLW | 266 | 8 | 1044 |
| PSTFPDLESEF | 95 | = | 1045 |
| PTTMNYPL | 72 | 8 | 1046 |
| PTTMNYPLW | 72 | 6 | 1047 |
| OAALSRKV | 901 | 8 | 1048 |
| OAALSRKVAEL | 106 | = | 1049 |
| OSPOGASSL | 63 | 6 | 1050 |
| RAIVETSY | 276 | . • | 1051 |
| RAIVETSY | 276 | . 6 | 1052 |
| RAIVETSYVKV | 276 | _ | 1053 |
| RARFDVTKAFM | 125 | | 1054 |
| ROHCKPEEGI | 90 | = | 1055 |
| NWILL ISS | . 69 | 6 | 1056 |
| SSLPTTMNYPL | 69 | | 1057 |
| SSLOLVEGI | 156 | 6 | 1058 |
| SSLOLVFGIEL | 156 | = | 1059 |
| SSSLOLVF | 155 | 8 | 0901 |
| SSSLQLVFGI | 155 | 10 | 1901 |
| SSSSTLVEV | 40 | 6 | 1062 |
| SSSSTLVEVTL | 40 | = | 1063 |
| SSSTLVEV | 41 | ∞ ' | 1064 |
| SSSTLVEVTL | 41 | 01 | 1065 |
| SSTLVEVTL | 42 | 6 | 9901 |
| STFPDLESEF | 96 | 0 · | 1901 |
| STLVEVTL | 43 | ∞ : | 890 |
| STLVEVTLGEV | 43 | _ : | 6901 |
| TSYVKVLHHM | 281 | ≘: | 0.01 |
| TSYVKVLHHMV | 281 | ≃ • | 1/01 |
| TTMNYPLW | 73 | 00 0 00 | 10/2 |
| VAELVHFL | 2 : | o 0 | 1074 |
| VAELVHILL | 5.0 | , I | 1075 |
| VTKAEMLGSV | 130 | 01 | 1076 |
| VTKAEMLGSVV | 130 | = | 1017 |
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Table XIV A Mage 2 B62 Supermotif Peptides Position

| | THE PARTY AND TH | 3 | |
|-------------------------|--|-----------------------|--------------|
| Sequence | Position | No. of Amino Acids | SEQ ID NO. |
| | | | |
| AISRKMVELV | 801 | 10 | 1078 |
| ALIETSYV | 277 | ∞ | 1079 |
| ALIETSYVKV | 777 | 01 | 1080 |
| CQDFFPVI | 143 | œ | 1801 |
| CQDFFPVIF | 143 | 6 | 1082 |
| DLESEFQAAI | 001 | 01 | 1083 |
| DLVQENYLEY | 249 | 01 | 1084 |
| DPACYEFLW | 265 | 6 | 1085 |
| ELSMLEVF | 224 | 8 | 9801 |
| ELVHFLLLKY | 115 | 10 | 1087 |
| EPVTKAEM | 128 | .8 | 1088 |
| EVFEGREDSV | 229 | 10 | 1089 |
| EVFEGREDSVF | 229 | = | 0601 |
| EVVEVVPI | 165 | ∞ | 1601 |
| EVVPISHLY | 168 | 6 | 1092 |
| EVVPISHLYI | 168 | 10 | 1093 |
| FLWGPRALI | 271 | 6 | 1094 |
| FPDLESEF | . 86 | ∞ | 1095 |
| FPVIESKASFY | 147 | .= | 9601 |
| FOANSRKM | 105 | . 0 | 1097 |
| FOAAISRKMV | 501 | . 01 | 8601 |
| GIEVVEVV | 163 | ∵ ∞ | 6601 |
| GIEVVEVVPI | 191 | 01 | 100 |
| OUTU | 880 | | 101 |
| CITCDNOW | 800 | 6 | 1102 |
| GLIIVLAI | 200 | . 6 | 1103 |
| GLLIIVLAII | 200 | 10 | 104 |
| GPRALIETSY | 274 | 10 | 1105 |
| GPRALIETSYV | 274 | = | 1106 |
| HPRKLLMQDLV | 241 | = | 1107 |
| IIVLAIIAI | 203 | 6 | 1108 |
| ILVTCLGLSY | 177 | 01 | 1109 |
| IVLAIIAI | 204 | ∞ | 011 |
| KIGGEPHI | 292 | œ | Ξ |
| KIGGEPHISY | 292 | 01 | 1112 |
| KIWEELSM | 220 | ∞ : | £ |
| KIWEELSMLEV | 240 | _ 0 | + |
| KLLMQDLV | 113 | o | 511 |
| NW CLVAR KVI HHTI KI | 285 | o 0 | 2112 |
| I FTSVVKV | 278 | · 6 | 118 |
| LIIVEAII | 202 | . ∞ | 6111 |
| LIIVLAIIAI | 202 | 10 | 1120 |
| LLGDNQVM | 681 | ∞ · | 1121 |
| LLIIVLAI | 201 | ∞ α | 1122 |
| LLIIVLAII | 701 | ~ | C711 |

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| Augland 201 11 1124 Augland 201 11 1125 OD VORBEY 224 11 1126 OD VORBEY 234 11 1126 OD VORBEY 234 11 1127 PERIOD 158 9 1136 PERIOD 16 11 1126 PERIOD 16 11 1126 PERIOD 16 11 1136 PERIOD 16 11 1136 PERIOD 9 1136 1136 PERIOD 9 1144 1144 PERIOD 9 1146 1146 PERIOD 9 1146 1146 PER | | | Amino Acids | |
|--|---|------------|-------------|------|
| 2.45 2.45 1.58 1.58 1.58 1.59 | ALAIIAI | 201 | 11 01 | 1124 |
| 245 246 158 158 160 160 160 160 160 160 160 160 160 160 | EPV | 120 | 2= | 1126 |
| 1.88 1.60 | ENY | 245 | | 1127 |
| 158 160 160 160 170 171 171 171 171 171 172 173 174 175 175 175 175 175 175 175 175 | Z. | 246 | 2 0 | 1128 |
| 45 66 66 66 66 66 66 66 66 66 66 66 66 66 | > | 25.8 | 10 | 1130 |
| 160 160 170 170 180 180 180 180 180 180 180 18 | | 45 | 6 | 1131 |
| 166 116 116 116 117 118 118 119 119 119 119 119 119 | | 160 | 80 | 1132 |
| 150 178 178 196 196 197 198 198 199 199 199 199 199 199 | <u>></u> | 091 | 01 | 1133 |
| 2116 178 287 196 197 198 198 199 199 199 199 199 199 | Λ, | 091 | = ‹ | 1134 |
| 250 196 196 196 197 198 198 199 119 129 129 139 139 139 139 139 139 130 130 130 130 130 130 130 130 | _ | 911 | 5 | 1135 |
| 196 196 196 197 198 198 199 199 199 199 199 199 199 199 | >- • | 250 | 5 | 1136 |
| 196 196 197 198 198 198 199 199 199 199 199 | | 8/1 | · • | 1138 |
| 247 88 89 89 80 61 111 129 159 159 159 160 170 180 180 190 190 190 190 190 190 190 19 | | 96 | • 0 | 1130 |
| 247.5 88 89 193 165 165 165 165 165 166 167 168 178 188 188 188 188 188 188 18 | | 96. | ^ 2 | 1140 |
| 89 89 89 61 61 171 188 189 64 189 180 180 180 180 190 190 190 190 190 190 190 19 | . > | 247 | <u> </u> | 141 |
| 89 171 61 65 65 65 189 180 189 190 190 190 190 190 190 190 19 | - 5 | 68 | . 6 | 1142 |
| 193 66 65 65 159 159 159 159 159 160 170 180 180 190 190 190 190 190 190 190 19 | | 68 | . 01 | 1143 |
| 171 65 65 128 159 159 159 250 64 64 64 65 65 65 66 66 67 138 138 139 139 139 | | 193 | := | 1144 |
| 65 148 159 159 159 159 159 159 160 170 180 180 190 190 190 190 190 190 190 19 | į | 121 | : 6 | 1145 |
| 65 148 159 159 159 160 170 180 190 190 190 190 190 190 190 19 | SSF | 19 | . = | 1146 |
| 148 159 159 159 169 179 184 184 189 189 189 180 180 180 180 180 180 180 180 180 180 | i F | 65 | = | 1147 |
| 129 159 8 8 159 15 | ~ | 148 | 10 | 1148 |
| 159 159 159 169 164 164 170 188 188 188 188 189 190 190 190 190 190 190 190 190 190 19 | ESV | 129 | = | 1149 |
| 159 159 36 36 194 194 194 260 260 260 27 27 27 27 27 280 280 290 290 290 290 290 290 290 290 290 29 | | 159 | 8 | 1150 |
| 159 194 194 194 195 260 260 27 237 138 138 149 140 150 160 17 18 19 19 19 19 19 19 19 19 19 19 | | 159 | 6 | 1151 |
| 36 194 194 195 260 260 64 64 64 64 138 138 149 149 150 160 170 180 190 190 190 190 190 190 190 19 | EV | 159 | = | 1152 |
| 194 194 260 96 64 64 138 138 138 149 190 190 190 190 190 190 190 19 | ۲۸ | 36 | = | 1153 |
| 194 266 96 64 64 64 138 138 138 10 10 10 10 139 139 139 | 5 | 194 | 10 | 1154 |
| 260 96 10 10 138 138 138 144 144 145 139 139 139 | ======================================= | 194 | = | 1155 |
| 259 259 64 64 138 138 138 198 199 149 139 139 | } ; | 260 | 10. | 1156 |
| 259 64 88 138 138 138 149 149 139 139 | £. | 96 | 10 | 1157 |
| 237 138 138 138 10 290 44 149 139 139 139 | ١CY | 259 | = | 1158 |
| 237 138 138 10 290 44 149 10 139 139 139 139 | | 2 8 | ∞ | 1159 |
| 138 9 290 10 44 10 149 9 286 8 139 8 | ,LM | 237 | = | 1160 |
| 138 10 290 10 44 10 149 9 286 8 139 8 | | 138 | 6 | 1161 |
| 290 10 10 149 286 8 8 139 139 9 139 9 139 9 139 139 139 139 1 | 11. | 138 | 01 | 1162 |
| 44 10 149 9 286 8 139 8 139 9 | | 290 | 10 | 1163 |
| 149 9 9 2 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 | > | 44 | 01 | 1164 |
| 286 8 139 8 139 9 | | 149 | 6 | 591 |
| 139 9 9 11 139 11 11 11 11 11 11 11 11 11 11 11 11 11 | | 286 | ∞ 6 | 9911 |
| 130 | | 139 | × 0 | 1011 |
| | ,,02 | 130 | ^ = | 1169 |

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| | Mage 2 B62 Supermotif Peptides | rmotif Peptides | |
|----------|--------------------------------|-----------------------|----------|
| Sequence | Position | No. of Amino Acids | SEQ ID N |
| KTGLLI | 195 | 6 | 1170 |
| KTGLIII | 195 | 01 | 1171 |
| KTGLLIIV | 195 | = | 1172 |
| SDPACY | 261 | 6 | 1173 |
| SDPACYEF | 261 | = | 1174 |
| HLYI | 170 | 80 | 1175 |
| HLYILV | 170 | 10 | 1176 |
| NYLEY | 251 | 8 | 7111 |
| NYLEYROV | 251 | = | 1178 |
| WPISHLY | 166 | = | 1179 |
| SHLY | 691 | ∞ | 1180 |
| SHLYI | 169 | 6 | 1811 |
| SHLYILV | 691 | = | 1182 |
| TCLGLSY | 176 | = | 1183 |
| LVFGI | 157 | 8 | 1184 |
| LVFGIEV | 157 | 10 | 1185 |
| LVFGIEVV | 157 | = | 1186 |
| VLHHTLKI | 283 | = | 1187 |
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| | Table XIV B Mage 3. B62 Supermotif Peptides | | |
|------------------------------|---|-----------------------|----|
| Sequence | Position | No. of Amino Acids | SE |
| ALSRKVAELV | 801 | 10 | ł |
| ALVETSYV | 277 | 8 | |
| ALVETSYVKV | 277 | <u>o</u> : | |
| DPACYEFLW DRIGHI VI | 265 170 | ∞ ∞ | |
| DPIGHLYIF | 170 | , o | |
| DPKKLLTQHF | 241 | 01 | |
| DPKKLLTQHFV | 241 | = • | |
| ELMEVDPI | 165 334 | oo oo | |
| ELSVEEVE ELVHELLIKY | 115 | ○ | |
| EMLGSVVGNW | 134 | 20 | |
| EPVTKAEM | 128 | 80 | |
| EVDPIGHLY | 168 | <u>ه</u> : | |
| EVDPIGHLYI | 168 | 2: | |
| EVDPIGHL YIF | 89 | <u> </u> | |
| EVFEGREDSI | 677 | 2 ∘ | |
| FLWGPRALV | 1/7 | o∧ ∝ | |
| FPULESEF | 50 105 | o o | |
| FVOENYI FV | 250 | , 6 | |
| GELMEVDPI | 163 | 10 | |
| GLLGDNQI | 188 | | |
| GLLGDNQIM | 188 | Φ. | |
| GLLIIVLAI | 200 | 6. | |
| GLLIVLAII | 200 | 2 5 | |
| OFRALVETSY CBB A I VETSYV | 417 VLC | 2 = | |
| UPRALVEISTV HISVODI HEW | 208 | 0 | |
| HISTORIA HEWA | 298 | 2 = | |
| HWYKISGGPHI | 289 | = | |
| IMPKAGLLI | 195 | 6 | |
| IMPKAGLLII | 195 | 10 | |
| IMPKAGLLIIV | \$61 | Ξ, | |
| KISGGPHI | 292 | ∞ ⊆ | |
| KISGGPHISY | 292 | ⊇ ∝ | |
| NIWEELSV WINTEL SM EV | 027 | ° = | |
| KIWEELSVLEV | 244 | ∞ | |
| KVAELVHF | 112 | · & | |
| KVLHHMVKI | 285 | 6 | |
| LIIVLAII | 202 | ∞ • | |
| LLGDNQIM | 189 | × × | |
| LLIIVI AII | 201 | o 0 | |
| LLIIVLAU | 121 | 10 | |
| | į | | |

| <i>j.</i> | · (| Ni | 15 |
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| - | Mage 3 B62 Supermotif Peptides | notif Peptides | |
|----------------|--------------------------------|-----------------------|------------|
| Sequence | Position | No. of Amino Acids | SEQ ID NO. |
| | | | |
| LLLKYKAKEPV | 120 | | 1234 |
| LLTQHFVQENY | 245 | _ | 1235 |
| LMEVDPIGHLY | 166 | = | 1236 |
| LPTTMNYPLW | 11 | 10 | 1237 |
| LQLVFGIELM | 158 | 10 | 1238 |
| LVETSYVKV | 278 | 6 | 1239 |
| LVEVTLGEV | 45 | 6 | 1240 |
| LVFGIELM | 160 | • | 1241 |
| LVFGIELMEV | 091 | 01 | 1242 |
| LVHFLLLKY | 116 | . 0 | 1243 |
| MLGSVVGNW | 135 | . 6 | 1244 |
| MIGSVVGNWOV | 135 | · = | 1245 |
| MPKAGLLI | 961 | ∵ ∞ | 1246 |
| MPKAGITI | 961 | ာ | 2721 |
| MPKAGITIV | 961 | \ C | 1547 |
| MVKISCOBLI | 280 | 2 5 | 957 |
| NOTE TO SECURE | 067 | | 6471 |
| NCEECOFSI F | 60 | ⊇: | 0571 |
| NÇIMPKAGLLI | <u> </u> | Ξ, | 1251 |
| PIGHLYIF | 171 | ∞ | 1252 |
| PQGASSLPTTM | 65 | = | 1253 |
| PVTKAEMLGSV | 129 | = | 1254 |
| QIMPKAGLLI | 194 | 10 | . 1255 |
| QIMPKAGLLII | 194 | = | 1256 |
| QLVFGIELM | 159 | 6 | 1257 |
| QLVFGIELMEV | 159 | = | 1258 |
| QVPGSDPACY | 260 | 10 | 1259 |
| ROVPGSDPACY | 259 | = | 1260 |
| SLPTTMNY | 70 | ∞ | 1261 |
| SLPTTMNYPLW | 70 | == | 1262 |
| SLOLVFGI | 157 | • | 1263 |
| SLOLVFGIELM | 157 | = | 1264 |
| SVYGNWOY | 38 | ∵ ∞ | 1265 |
| SVVGNWOYF | 200 | . 6 | 1266 |
| SVVGNWOYFF | 38 | 01 | 1267 |
| TLVEVTLĜEV | 44 | 01 | 1268 |
| TMNYPLWSQSY | 74 | = | 1269 |
| TOHFVOENY | 247 | 6 | 1270 |
| VLHHMVKI | 286 | . ∞ | 1271 |
| VPGSDPACY | 261 | . 6 | 1272 |
| VPGSDPACYEF | 261 | . = | 1273 |
| VOENYLEY | 251 | ∞ | 1274 |
| VOENYLEYROV | 251 | = | 1275 |
| VVGNWQYF | 139 | ∞ | 1276 |
| VVGNWQYFF | 139 | 6 | 1277 |
| VVGNWQYFFPV | 139 | = | 1278 |
| WQYFFPVI | 143 | ∞ | 1279 |

| į. | • | ~·· | 13/ | a |
|----|-------|-----|-----|-----------|
| Ĺ |) | | | Table XIV |

| Mage 3 B62 S | Mage 3 B62 Supermotif Peptides | |
|--------------|--------------------------------|--------|
| Position | No. of Amino Acids | OI ČES |
| 143 | 6 | 1280 |
| 176 | = | 1281 |
| 77 | ∞ | 1282 |
| 301 | 8 | 128 |
| 283 | ∞ | 128 |
| 283 | 6 | 1285 |
| 283 | | 1286 |

| | ia | 10 |
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| P. | _ | |

| | 2 | lage 4 AUL Moth Peptides with Binding | <u>Data</u> | |
|-------------|----------|---------------------------------------|-------------|------------|
| Sequence | Position | No. of Amino Acids | A*0101 | SEQ ID NO. |
| ASSESTTINY | 89 | 10 | 0.1700 | 1287 |
| GASSFSTTINY | 29 | = | 0.0047 | 1288 |
| GGEPHISY | 294 | ∵∞ | -0.0021 | 1289 |
| IFSKASEY | 150 | ∞ | 0.0023 | 1290 |
| LMQDLVQENY | 246 | 10 | 0.0450 | 1291 |
| MQDLVQENY | 247 | 6 | 1.5000 | 1292 |
| PGSDPACY | 262 | ∞ | -0.0021 | 1293 |
| PRALIETSY | 275 | 6 | -0.0006 | 1294 |
| SFSTTINY | 70 | • | -0.0021 | 1295 |
| SSFSTTINY | 69 | 6 | 0.0430 | 1296 |
| VQENYLEY | 251 | 8 | -0.0021 | 1297 |
| VTCLGLSY | 179 | ∞ | | 1298 |
| VVEVVPISHLY | 991 | = | 0.2000 | 1299 |

| į | W.K | 5 |
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| | | 7 |

| | SEQ ID NO. | 1300 1302 1303 1304 1306 1306 1309 1311 1312 1313 1313 | 1315 |
|--|-----------------------|--|----------|
| Data | A*0101 | 2,6000 0,1100 18,0000 0,0390 0,0390 0,0390 0,0020 0,0020 0,0020 0,0021 0,0021 0,0021 0,0021 0,0031 | -0.0021 |
| Table XV B Mage 3 A01 Motif Peptides with Binding Data | No. of Amino Acids | 5 ≈ 9 = 9 5 9 5 = 5 ≈ 9 9 = | 80 |
| a | Position | 68 179 168 137 137 136 166 166 262 262 275 74 | 251 |
| | Sequence | ASSLPTTMNY ATCLGLSY EVDPIGHLY GASSLPTTMNY GSVYGNWQY IFATCLGLSY ISGGPHISY LGSVYGNWQY LMEVDPIGHLY LMEVDPIGHLY LMEVDPIGHLY PGSDPACY PRALVETSY SSLPTTMNY TMNYPLWSQSY | VQENYLEY |

| lt | M. | · 1 |
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| L | | |

| - | | Mage 2 A03 Motif Peptides with Binding Data | Data | |
|-------------|----------|---|---------|------------|
| Sequence | Position | No. of Amino Acids | A*0301 | SEQ ID NO. |
| AADSPSPPH | 55 | 6 | 0.0003 | 1316 |
| ACYEFLWGPR | 267 | . 01 | 0.0032 | 1317 |
| ACYEFLWGPRA | 267 | = | | 1318 |
| ADSPSPPH | 56 | ∞ | | 1319 |
| AIEGDCAPEEK | 210 | = | 0.0009 | 1320 |
| AllAlEGDCA | 207 | 10 | | 1321 |
| AISRKMVELVH | 801 | = | | 1322 |
| ALGLVGAQA | 22 | 6 | 0.0003 | 1323 |
| ALGLVGAQAPA | 22 | = | | 1324 |
| ALIETSYVK | 277 | 6 | 0.0810 | 1325 |
| ASEYLQLVF | 154 | 6 | 0.0002 | 1326 |
| ASSFSTTINY | 89 | 01 | 0.000 | 1327 |
| ATEEQQTA | 32 | 80 | | 1328 |
| DFFPVIFSK | 145 | 6 | 0.0002 | 1329 |
| DFFPVIFSKA | 145 | 10 | | 1330 |
| DLESEFQA | 100 | ∞ | | 1331 |
| DLESEFQAA | 100 | 6 | | 1332 |
| DLVQENYLEY | 249 | 01 | | 1333 |
| DLVQENYLEYR | 249 | = | 0.0047 | 1334 |
| DSVFAHPR | 236 | 8 | -0.0004 | 1335 |
| DSVFAHPRK | 236 | 6 | 0.0021 | 1336 |
| EALGLVGA | 21 | ∞ | | 1337 |
| EALGLVGAQA | 21 | 01 | 0.0003 | 1338 |
| EDSVFAHPR | 235 | 6 | | 1339 |
| EDSVFAHPRK | 235 | 10 | | 1340 |
| EFLWGPRA | 270 | 8 | | 1341 |
| EFQAAISR | 104 | 80 | | 1342 |
| EFQAAISRK | 104 | 6 | 0.0002 | 1343 |
| EGDCAPEEK | 212 | 6 | 0.0002 | 1344 |
| EGLEARGEA | 4 | 6 | 0.0003 | 1345 |
| EGREDSVF | 232 | • | | 1346 |
| EGREDSVFA | 232 | 6 | | 1347 |
| EGREDSVFAH | 232 | 10 | | 1348 |
| ELSMLEVF | 224 | · 00 | | 1349 |
| ELSMLEVFEGR | 224 | · = | 0.0016 | 1350 |
| ELVHFLLLK | 115 | : 6 | 0.0045 | 1351 |
| ELVHFLLLKY | 115 | . 01 | 0,0066 | 1352 |
| ELVHFLLLKYR | . 113 | := | 0.0011 | 1353 |
| EMLESVLR | 134 | ; oc | -0.000 | 1354 |
| ESEFQAAISR | 102 | . 0 | 0.0002 | 1355 |
| ESEFŐAAISRK | 102 | = | 0.0010 | 1356 |
| ESVLRNCQDF | 137 | 10 | 0.0002 | 1357 |
| ESVLRNCQDFF | 137 | = | | 1358 |
| ETSYVKVLH | 280 | 6 | | 1359 |
| ETSYVKVLHH | 280 | 01 | | 1360 |
| EVFEGREDSVF | 229 | = | | 1361 |

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| <u>(</u> | | |

| | Mage 2. A | Table XVI A Mage 2 A03 Motif Reptides with Binding Data | A *0301 | ON CI CAS |
|--|-----------|---|---------|------------|
| Sequence | Position | No. ot Amino Acids | A*USUI | SEQ ID NO. |
| EVTLGEVPA | 47 | 6 | 0.0003 | 1362 |
| EVTLGEVPAA | 47 | 10 | 0.0003 | 1363 |
| EVVEVVPISH | 165 | 01 | 0.0002 | 1364 |
| EVVPISHLY | 168 | 6 | 0.0002 | 1365 |
| FFPVIFSK | 146 | · | | 1366 |
| FFPVIFSKA | 146 | 0 | 0.0003 | 1367 |
| FLLLKYRA | 677 | 00 (| | 1368 |
| FLLLKYKAK | 9.1 | 6: | | 1369 |
| FSLLINYILWK | - 17 | = = | 0.010 | 1370 |
| CASSISITION | 33 | _ • | | 1372 |
| GDCALEEN | 161 | ≎ ∝ | | 1373 |
| GEFFUSY | 294 | o oc | | 1374 |
| GUST TIEST | | · • | | 1375 |
| GLLGDNOVMPK | 882 | · = | 0.0780 | 1376 |
| GLLIIVLA | 200 | . 00 | | 1377 |
| GLIIVLAIIA | 200 | -= | | 1378 |
| GLYGADAPA | 24 | : o | 0.0003 | 1379 |
| GSDPACYEF | 263 | \ 0 | | 1380 |
| GSSNOEEEGPR | 86 | . == | -0.0002 | 1381 |
| HCKPEEGLEA | 36 | . 2 | 0.0003 | 1382 |
| HCKPEEGLEAR | . 0 | : = | | 1383 |
| HFLLLKYR | 118 | ∵∞ | | 1384 |
| HFLLLKYRA | 118 | 6 | 0.0016 | 1385 |
| HFLLLKYRAR | 118 | 01 | 0.0014 | 1386 |
| HISYPPLH | 298 | ∞ | | 1387 |
| HISYPPLHER | 298 | 10 | 0.0074 | 1388 |
| HISYPPLHERA | 298 | = | | 1389 |
| HSPQGASSF | 63 | 6 | 0.0002 | 1390 |
| HTLKIGGEPH | 289 | 01 | | 1391 |
| IAIEGDCA | 209 | ∞ | | 1392 |
| IFSKASEY | 150 | ∞ | | 1393 |
| IGGEPHISY | 293 | 6 | | 1394 |
| IIAIEGDCA | 208 | • | | 1395 |
| IIVLAIIA | 203 | × ; | 2000 | 965 |
| ILVTCLGLSY | 171 | 01 | 0.0036 | 1397 |
| ISRKMVELVH | 601 | 0: | 0.0002 | 1398 |
| ISKKMVELVHF | 601 | <u> </u> | 0.0340 | 1400 |
| ISTERATED TO THE STATE OF THE S | 299 | ٠ <u>-</u> | 0,000 | 1401 |
| KAEMI FSVI R | 133 | 2 5 | 0 0002 | 1402 |
| KASEVI OI VE | 153 | 2 = | 0.0002 | 1403 |
| KIGGEPHISY | 292 | 20 | | 1404 |
| KMVELVHF | 112 | ∵ ∞≎ | | 1405 |
| KTGLLIIVLA | 198 | 01 | | 1406 |
| KVLHHTLK | 285 | ∞ | 0.0053 | 1407 |
| | | | | |

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| | | | 143 | |
|--|-------------|-------------|---|--------------|
| Carrience | Position | No of | A*0301 | SEO ID NO. |
| and the second s | | Amino Acids | | |
| LAIIAIEGDCA | 206 | = | | 1408 |
| LGDNQVMPK | 190 | : 6 | 0.0002 | 1409 |
| LGLVGAQA | 23 | •• | | 1410 |
| LGLVGAQAPA | . 23 | 01 | 0.0003 | 1411 |
| LIETSYVK | 278 | ∞ | -0.0004 | 1412 |
| LIETSYVKVLH | 278 | = 4 | | 1413 |
| LIIVLAIIA | 707 | ~ 5 | 0000 | * |
| LLGDNQVMPK | 189 | 0.5 | 0.0093 | 1413 |
| LLIKYRAR | 120 | ≥ ∞ | 6000 0- | 1417 |
| LLMODILVOENY | 245 | · = | | 1418 |
| LMODLVOENY | 246 | :01 | | 1419 |
| LSMLEVFEGR | 225 | 01 | -0.0004 | 1420 |
| LVEVTLGEVPA | 45 | = | | 1421 |
| LVGAQAPA | . 25 | ∞ | | 1422 |
| LVHFLLLK | 911 | œ (| 0.0290 | 1423 |
| LVHFULLKY | 911: | σ; | 0.0430 | 1424 |
| LVHFLLLKYK | 911 | 2: | 0.0200 | 1425 |
| LVHFLLLKYKA | 350 | <u> </u> | | 1428 |
| LVCENT ELEI | 250 | » (- | 0.0027 | 1428 |
| LVTCLGLSY | 178 | 2 0 | | 1429 |
| MFPDLESEF | 76 | . 0 | 0.0002 | 1430 |
| MFPDLESEFQA | . 46 | | , | 1431 |
| MLEVFEGR | 227 | ∞ : | -0.0009 | 1432 |
| MVELVHFLLLK | = : | = : | 0.0200 | 1433 |
| DA A DEBERBH | 77 77 | 2.5 | 0.0002 | 1434 |
| PACYEE WGPR | 266 | 2 = | 6000 0- | 1436 |
| PATEEOOTA | 3] | - 6 | | 1437 |
| PDLESEFOA | .66 | . 6 | 0.0003 | 1438 |
| PDLESEFÓAA | 66 | 10 | 0.0003 | 1439 |
| PGSDPACY | 262 | ∞ | | 1440 |
| PGSDPACYEF | 262 | 10 | | 1441 |
| PLEQRSQH | 7 | ∞ : | *************************************** | 1442 |
| PLEQRSQHCK | 7 | 0. | 0.0003 | 1443 |
| PLHERALR | 303 | ∞ 5 | -0.0009 | 1444 |
| PALFRA CEV | 96 | 2 5 | 0.0160 | 1446 |
| OAPATEFOOTA | 29 | 2 = | 2000 | 1447 |
| ODFFPVIF | 144 | : ∝ | | 1448 |
| ODFFPVIFSK | 144 | , <u>e</u> | 0.0002 | 1449 |
| QDFFPVIFSKA | 144 | == | | 1450 |
| QDLVQENY | 248 | ∞ ; | | 1451 |
| QDLVQENYLEY | 248 | Ξ• | | 1452 |
| CVrusura | 707 | ro. | | 7) - |

| (i | 10 | in the |
|----|----|--------|
| 1 | | |

| | SEQ ID NO. | 1454 | 1455 | 1450 | 458 | 1459 | 1460 | 1461 | 1463 | 1464 | 1465 | 1466 | 1467 | 1468 | 1469 | 1470 | 1472 | 1473 | 1474 | 1475 | 1476 | 147/ | 14/6 | 1480 | 1481 | 1482 | 1483 | 1484 | 1485 | 1487 | 1488 | 1489 1490 | |
|---|-----------------------|------------|------------------------|----------|------------|------------|------------|----------|-----------|-----------|------------|------------|----------|-----------|------------|----------|----------|-----------|----------|-----------|------------|-------------|-----------|----------|-----------|----------|----------|-----------|-----------|----------|-------------|---------------------------|---|
| | A*0301 | | 00000 | -0.000 | | 0.0003 | 0.0002 | | 0.0020 | | 0.0002 | 0.0014 | 0.1410 | 0.0002 | 0.0002 | 0.0140 | | | | 0.5900 | 0.0800 | | 0.0810 | | 0.0002 | | | 0.0003 | 0.0007 | | | 0.0033 | |
| Table XVIA Mage 2. A03 Motif Peptides with Binding Data | No. of Amino Acids | 01 | ∞⊆ | ⊇ ∞ | > 6 | 10 | 10 | ∞.∞ | o 0 | 6 | 10 | 01 | ∞ . | o : | 2 (| > ∝ | , ∞ | . 6 | ∞ | 6 | 6 : | 01 | _ 0 | \ ∞ | . 6 | ∞ | ∞ | 6 | o : | ~ ∞ | ·= | 11 01 | • |
| | Position | 260 | 976 | 125 | 125 | 61 | 9 | 264 7 | 226 | 69 | 87 | 72 | 237 | 38 | 85. | <u>7</u> | 49 | 290 | 281 | 281 | 73 | 730 | 149 | 139 | 139 | 179 | 48 | 48 | 99 2 | 69 | 273 | 176 283 | |
| | Sequence | QVPGSDPACY | KALIEISY PALIETSYVK | RAREPVTK | RAREPUTKA | RGEALGLVGA | KMFPDLESEF | SDPACYEF | SMLEVFEGR | SSFSTTINY | SSNQEEEGPR | STTINYTLWR | SVFAHPRK | SVLRNCQDF | SVLKNCQUFF | TINYTUWE | TLGEVPAA | TLKIGGEPH | TSYVKVLH | TSYVKVLHH | TINYTLWR | VFEGREDS VF | VIESKASEV | VLRNCODF | VLRNCQDFF | VTCLGLSY | VTLGEVPA | VTLGEVPAA | VVEVVPISH | VVPISHLY | WGPRALIETSY | YILVTCLGLSY YVKVLHHTLK | |

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|---|-------------|----|--|
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| PRA 2017 PRA 20 | | | Table XVI B Mage 3 A03 Motif Peptides with Binding Data | Data | |
|--|--|------------------|--|---|-----------------|
| 267 107 267 10 00032 267 11 10 00003 267 11 10 00003 268 11 11 00003 272 11 11 00003 273 11 10 00003 274 11 10 00003 275 11 10 | Sequence | Position | No. of Amino Acids | | SEQ ID NO. |
| PRA 257 PRA 267 PRA 26 | AALSRKVA | 107 | 80 | | 1491 |
| PRA 1967 A A 227 A | ACYEFLWGPR | 267 | . 01 | 0.0032 | 1492 |
| A A 2070 A A 2077 A 2077 A | ACYEFLWGPRA | 267 | = | | 1493 |
| A 207 APA 227 | AGLLIIVLA | 166 | 6 | 90000 | 1494 |
| AAA 222 AAA 222 AAA 222 AAA 222 AAA 222 BAB B B B B B B B B B B B B B B B B B B | AIIAREGDCA | 207 | . 01 | | 1495 |
| AAA 122 AAA 128 AAA 129 AAA 129 AAA 129 AAA 129 AA 121 AAA 122 AA 124 AA | ALGLVGAQA | 22 | 6 | 0.0003 | 1496 |
| V.Y.H. 227 V.Y. 227 V.Y. 227 V.Y. 154 V.Y. 168 V.Y. | ALGLVGAQAPA | 22 | 11 | | 1497 |
| Y.Y. 687 Y.Y. 687 154 175 175 175 175 175 175 17 | ALSRKVAELVH | 108 | = | | 1498 |
| 174 154 10 0 0 0 0 0 0 0 0 | ALVETSYVK | 277 | 6 | 0.0270 | 1499 |
| 154 154 157 158 158 159 | ASSLPTTMNY | 89 | 01 | 0.000 | 1500 |
| 179 179 179 170 170 170 170 170 170 170 170 170 170 | NSSSLQLVF | 154 | 6 | 0.0011 | 1501 |
| 132 136 137 138 139 139 130 130 130 130 130 130 130 130 130 130 | \TCLGLSY | 179 | • | | 1502 |
| 100 8 100 8 100 10 | TEEOEAA | 32 | • • | | 1503 |
| 236 236 236 237 238 238 239 239 239 239 239 239 239 239 239 239 | DLESEFOA | 100 | • | | 1504 |
| 256 256 257 258 259 251 251 251 252 252 253 253 253 253 253 253 254 254 254 254 254 258 258 258 258 258 258 258 258 258 258 | OI ESEFOAA | 901 | · • | | 1505 |
| 256 27 28 28 29 21 21 21 21 21 22 23 235 24 24 24 24 254 254 258 258 258 258 268 27 27 28 28 28 28 29 20 20 20 20 20 20 20 20 20 20 20 20 20 | SILGOPK | 236 | \ ox | -0 0004 | 9051 |
| 21 23 235 235 236 237 238 238 239 240 104 104 104 104 105 107 107 108 109 100003 100003 100003 100003 100003 100003 100003 100003 100003 111 112 113 114 115 116 117 118 119 119 110 110 110 111 111 111 | SILGDPKK | 236 | | -0.0003 | 1507 |
| 213 225 225 225 227 227 227 227 227 227 227 | ALGI VGA | <u> </u> | \ 0 | 00000 | 1508 |
| 235 235 236 237 238 104 104 104 104 104 105 106 107 107 107 107 107 108 108 108 108 108 108 108 108 108 108 | 75 C V C V C V C V C V C V C V C V C V C | ; , ; | o <u>S</u> | 0.0003 | 0051 |
| 235 270 8 104 104 105 8 8 0 00003 270 8 114 105 115 115 115 115 117 118 119 119 119 119 119 119 119 119 119 | DSII GDPK | 2.5 | 2 o | 0.0003 | 0151 |
| 270 270 104 104 105 106 107 108 8 8 00002 109 114 109 10003 | DOLL GROKK | 235 | ` = | 0.000 | 1151 |
| 104 8 8 0.0002 105 104 11 0.0002 115 10 0.0003 115 11 0.0003 117 11 0.0003 118 119 0.0002 119 0.0002 110 0.0002 110 0.0002 110 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 111 0.0003 | ESTECOL INC | 270 | 2 ∞ | 6000:0 | 1512 |
| 104 9 0 0.0002 212 14 9 9 0.0003 214 8 8 0.0003 224 8 8 0.0003 224 8 8 0.0003 224 11 0.0003 225 115 10 0.0005 226 10 10 0.0005 227 10 0.0002 228 9 0.0003 228 9 0.0003 228 9 0.0003 228 9 0.0003 238 9 0.0003 247 10 0.0003 258 9 0.0003 258 9 0.0003 258 9 0.0003 258 9 0.0003 258 9 0.0003 258 9 0.0003 258 9 0.0003 258 9 0.0003 | EO A L CB | 27- | 0 0 | | 1513 |
| 104 111 0.0002 124 8 8 0.0003 1254 8 8 0.0003 1254 8 8 0.0003 115 11 0.0005 115 11 0.0005 116 11 0.0005 117 11 0.0002 118 9 0.0003 119 8 0.0003 119 8 0.0003 | 100 A 100 V | | • • | ,000 | 6161 |
| 14 9 0.0002 14 9 0.0003 165 8 8 0.0003 17 9 0.0003 11 0.0004 11 0.0004 11 0.0004 11 0.0002 10 0.0002 10 0.0002 10 0.0002 10 0.0003 11 0.0003 12 0.0003 13 0.0003 14 0 0.0003 16 0.0003 17 0 0.0003 18 0 0.0003 | FOALSBY A | 5 3 | ^ = | 0.0002 | + C |
| 212 14 9 0 00002 224 8 8 0 00003 224 8 8 0 00003 115 10 000045 115 10 00005 115 11 00002 102 10 10 00002 280 9 0 00002 168 9 0 00003 168 11 0 00003 178 9 0 00003 178 9 0 00003 178 9 0 00003 179 9 0 00003 179 9 0 00003 | FLAALSKA VA | 2 6 | = . | *************************************** | CICI |
| 14 9 9 0,0003 15 10 0,0003 115 11 0,0004 115 11 0,0001 102 10 0,0002 103 10 0,0002 104 10 0,0003 105 10 0,0003 106 10 0,0003 107 108 8 0,0003 108 109 0,0003 109 0,0003 109 0,0003 119 119 109 119 119 109 119 119 119 110 110 110 111 111 111 112 113 114 113 115 115 114 115 115 115 115 115 116 117 117 117 118 118 118 118 118 119 119 118 119 119 118 119 118 118 119 119 118 119 118 119 1 | GDCAPEEK | 212 | 6 | 0.0002 | 9151 |
| 224 8 8 -0.0003 224 11 0.0003 225 115 11 0.0004 226 115 11 0.0005 280 280 9 9 0.0002 280 9 9 0.0003 280 9 9 0.0003 280 9 9 0.0003 280 11 0.0003 280 9 0.0003 280 11 0.0003 280 11 0.0003 | GLEARGEA | 4 | 6 | 0.0003 | 1517 |
| 224 111 -0.0009 115 9 0.0045 116 100 117 100 118 100 119 100 119 119 119 119 119 119 119 119 119 119 | LMEVDPIGH | 165 | 01 | 0.0003 | 8131 |
| 224 111 | LSVLEVF | 224 | ∞ | | 1519 |
| 115 9 0,0045 115 10 0,0006 102 10 0,0002 103 10 0,0002 104 10 0,0003 105 10 0,0003 106 10 0,0003 107 10 0,0003 108 109 0,0003 109 0,0003 109 0,0003 119 119 100 119 119 110 119 110 110 110 110 110 111 110 110 111 111 110 112 113 110 113 114 115 115 115 115 116 117 117 117 118 118 118 118 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 118 119 119 119 119 119 | :LSVLEVFEGR | 224 | = | -0.0000 | 1520 |
| 115 10 0.0066 102 11 0.0001 103 11 0.0002 280 9 0.0002 168 11 0.0002 168 11 0.0003 178 9 0.0003 178 8 0.0003 179 9 0.0003 170 10 0.0003 171 10 0.0003 172 173 174 173 174 175 174 175 175 175 175 175 176 177 177 177 177 177 178 8 0.0003 179 170 0.0003 170 170 0.0003 171 172 173 173 174 175 174 175 175 175 175 175 175 175 1 | LVHFLLLK | 115 | 6 | 0.0045 | 1521 |
| 115 117 0,0011 102 10 10 0,0002 280 9 9 0,0002 168 9 0 0,0002 168 11 0 0,0003 178 9 0,0003 178 8 0,0003 179 9 0,0003 | LVHFLLLKY | 115 | 10 | 0.0066 | 1522 |
| RK 102 10 0,0002 RK 102 11 0,0002 RK 280 9 0,0002 H 280 10 0,0002 F 47 9 0,0003 A 47 10 9 0,0003 A 178 9 0,0003 A 178 9 0,0003 A 178 9 0,0003 B 146 8 0,0003 | LVHFLLLKYR | 115 | = | 0.0011 | 1523 |
| RK 102 II 0.0002 H 280 9 0.0002 H 168 9 0 0.0003 F 47 9 9 0.0003 A 47 9 9 0.0003 I 146 8 8 0.0003 I 15 9 0.0003 | SEFQAALSR | 102 | 10 | 0.0002 | 1524 |
| H 280 9 0.0002 H 168 9 9 0.0002 F 168 11 0.0003 A 47 9 9 0.0003 178 9 0.0003 146 8 0.0003 119 8 0.0003 | SEFQAALSRK | 102 | = | 0.0002 | 1525 |
| H 280 10 0.0002 168 9 0 0.0002 168 11 0 0.0003 A 47 9 9 0.0003 A 6 178 9 9 0.0003 146 8 0 0.0003 119 8 8 0.0003 | TSYVKVLH | 280 | 6 | | 1526 |
| F 168 9 0.0002 168 11 11 0.0003 17 10 0.0003 178 9 0.0003 146 8 8 0.0003 119 1 | TSYVKVLHH | 280 | 10 | | 1527 |
| F 168 | VDPIGHLY | 168 | 6 | 0.0002 | 1528 |
| 47 9 0.0003 4 47 10 0.0003 178 9 0.0003 146 8 0.0003 119 8 | VDPIGHLYIF | 168 | = | | 1529 |
| A 47 10 0.0003 178 9 0.0003 146 8 0.0003 146 9 0.0003 | VTLGEVPA | 47 | : 6 | 0.0003 | 1530 |
| 178 9 0.0003 146 8 0.0003 146 9 0.0003 | VTLGEVPAA | 47 | 01 | 0.0003 | 1531 |
| 146 8 0.0003 146 9 0.0003 159 8 | ATCLGLSY | 178 | : 6 | 0.0003 | 1532 |
| 146 9 0.0003 119 8 | FPVIFSK | 146 | . oc | | 1533 |
| 88 611 | FPVIFSKA | 146 | • • | 0.0003 | 1534 |
| 0 0 0 1 | HIKVRA | 910 | . 00 | | 1535 |
| | 1 1 1 V V D A D | 27 | > C | | 9531 |
| | | | | | |

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| - | | ABDE AVLE Mage 3 A03 Motif Peptides with Binding Data | | |
|--------------------------|-------------|---|---|------------|
| Sequence | Position | No. of Amino Acids | A*0301 | SEQ ID NO. |
| SVOENXI EX | 750 | C | | 1522 |
| FVQENYLEYR | 250 | , 10 | 6000.0 | 1538 |
| GASSLPTTMNY | 29 | := | | 1539 |
| GDCAPEEK | 213 | ∞ : | | 1540 |
| GUNQIMPK | <u> </u> | >> | | 1541 |
| GDPK11 TOH | 191 | ۍ <u>د</u> | 0.0003 | 1542 |
| GDPKKI I TOHE | 240 | 2 = | 0.000.0 | 247 |
| GGPHISYPPLH | 295 | | | 1545 |
| GLEARGEA | 15 | : ∞ | | 1546 |
| GLLGDNQIMPK | 188 | · = | 0.1300 | 1547 |
| GLLIIVLA | 200 | 8 | | 1548 |
| GLLIVLAIIA | 200 | = | | 1549 |
| GLVGAQAPA | 24 | 6 | 0.0003 | 1550 |
| GSDPACYEF | 263 | 6 | | 1551 |
| GSVGNWQY | 137 | 6 | | 1552 |
| GSVVGNWQYF | 137 | 01 | 0.0020 | 1553 |
| GSVGRWQYFF | / <u>s</u> | = : | *************************************** | 1554 |
| HCNFEEULEA | ~ c | 2 : | 0.0003 | 555 |
| UCI I KVD | 911 | | | 000 |
| HELECKIN A | 0 - 1 | ∞ α | 31000 | /551 |
| HELLENINA | 011 | ~ ⊆ | 0.0010 | 1550 |
| HEVDENYLEY | 249 | | ± 20.0 | 1560 |
| HFVOENYLEYR | 249 | 2 = | | 1861 |
| HISYPPLH | 298 | : ∝ | | 1562 |
| HMVKISGGPH | 289 | . 02 | | 1563 |
| IAREGDCA | 509 | . ∞ | | 1564 |
| IFATCLGLSY | 171 | 10 | 0.0005 | 1565 |
| IGHLYIFA | 172 | ∞ | | 1566 |
| IIAREGICA | 208 | 6 | | 1567 |
| IIVLAIIA | 203 | ∞ | | 1568 |
| INCORTIEN | 203 | ο (| 0.0069 | 1569 |
| I SIN PIN IN | 207 | . · | 0.0003 | 5/2 |
| KAGI IIVI A | * 07 108 | o <u>C</u> | 0.00.0 | 1751 |
| K A SSSI OI VE | 251 | 2 5 | 0 0003 | 1573 |
| KINGGPHISY | 262 | 2 5 | 00000 | 1574 |
| KVAELVHF | 112 | 2 ∞ | | 1575 |
| KVLHHMVK | 285 | • •• | 0.0580 | 1576 |
| LAIIAREGDCA | 506 | = | | 1577 |
| LGDNQIMPK | 190 | 6 | | 1578 |
| LGDNQIMPKA | <u>8</u> | 01 | 0.0003 | 1579 |
| LGDPKKLLIQH | 239 | • | | 1580 |
| LOLVOAÇA I GI VGADAPA | 2 % | ø <u>C</u> | 0 0003 | 1587 |
| | ; | | | 2 |

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| | W | Table XVL B Mage 3 A03 Motif Peptides with Binding Data | | |
|-------------|------------|---|--|------------|
| Sequence | Position | No. of Amino Acids | A*0301 | SEQ ID NO. |
| I GSVVGNWOV | 136 | 10 | 0.0003 | 1583 |
| LGSVVGNWQYF | 136 | | | 1584 |
| LIIVLAIIA | 202 | 6 | | 1585 |
| LIIVLAIIAR | 202 | 01 | 0.0280 | 1586 |
| LLGDNQIMPK | 681 | 01 | 0.0200 | 1587 |
| LLGDNQIMPKA | 681 | = \$ | | 1288 |
| LLINGALIA | 107 | 2 = | 1,000,0 | 1590 |
| LLIIVLAIIAR | 120 | = ∝ | 0.000 | 1951 |
| LITOHEVOEN | 245 | o = | \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\ | 1592 |
| LMEVDPIGH | 991 | : 0 | 0.0002 | 1593 |
| LMEVDPIGHLY | 166 | = | | 1594 |
| LSRKVAELVH | 601 | 10 | 0.0002 | 1595 |
| LSRKVAELVHF | 109 | = | | 1596 |
| LSVLEVFEGR | 225 | 01 | -0.0006 | 1597 |
| LTQHFVQENY | 246 | 01 | 0.0003 | 866 |
| LVETSYVK | 278 | ∞ ; | -0.0004 | 6601 |
| LVEISYVKVLH | 2/8 | =; | | 0091 |
| LVEVILGEVPA | . 45 7. | <u></u> - | | 1001 |
| LVGAQAPA | 3.5 | × 0 | 08000 | 1602 |
| LVHFLLLR | 011 | × | 0.0290 | 1604 |
| LVELLENI | 911 | λ <u>-</u> | 0.0430 | 5091 |
| LVHFLLLKYRA | 116 | 2 = | | 9091 |
| MLGSVVGNWOY | 135 | == | | 1607 |
| MVKISGGPH | 290 | : 6 | 0.0003 | 8091 |
| PACYEFLWGPR | 596 | = | -0.0009 | 1609 |
| PATEEQEA | 31 | 8 | | 1610 |
| PATEEQEAA | 31 | 6 | 0.0003 | 191 |
| PDLESEFQA | 66 | 6 | 0.0003 | 1612 |
| PDLESEFQAA | 66 | 01 | 0.0003 | 1613 |
| PDPPQSPQGA | 59 | 10 | 0.0003 | 1614 |
| PGSDPACY | 262 | ∞ : | | 5191 |
| PGSDPACYEF | 262 | 10 | | 919 |
| PIGHLYIF | <u> </u> | ∞ (| | /191 |
| PIGHLYIFA | 171 | o | | 810. |
| PLEQRSQH | 7 7 | · · | 0 | 6191 |
| PLECKSOHCK | 7 | 2 € | 0.000 | 0791 |
| PLHEW VLK | 50 50 | × I | -0.000 | 1701 |
| CALICACIA | 25 401 | _ 0 | | 1623 |
| OAPATEROFA | 26 | · 01 | 0.0003 | 1624 |
| OAPATEEOEAA | : £2 | := | | 1625 |
| OVPGSDPA | 260 | : ∞ | | 1626 |
| ÓVPGSDPACY | 260 | 10 | | 1627 |
| RALVETSY | 276 | œ | | 8791 |

| ļ. | NO. | |
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| - | | Table XVI B | | |
|-------------|----------|---|---------|------------|
| - | | Mage 3 A03 Motif Peptides with Binding Data | | |
| Sequence | Position | No. of Amino Acids | A*0301 | SEQ ID NO. |
| RALVETSYVK | 276 | 01 | 0.0190 | 1629 |
| RAREPVTK | 125 | : ∞ | 6000'0- | 1630 |
| RAREPVTKA | 125 | 6 | | 1631 |
| RGEALGLVGA | 61 | 01 | 0.0003 | 1632 |
| SDPACYEF | 264 | ∞ | | 1633 |
| SGGPHISY | 294 | 8 | | 1634 |
| SILGDPKK | 237 | 8 | 6000'0- | 1635 |
| SLPTTMNY | 70 | • | | 1636 |
| SSLPTTMNY | 69 | 6 | | 1637 |
| SSSLOLVF | 155 | 8 | | 1638 |
| STFPDLESEF | 96 | 10 | 0.0002 | 1639 |
| SVLEVFEGR | 226 | 6 | 0.0003 | 1640 |
| SVVGNWOY | 138 | • • | | 1641 |
| SVVGNWOYF | 138 | . 6 | 0.0002 | 1642 |
| SVVGNWOYFF | 138 | 10 | 0.0085 | 1643 |
| TFPDLESEF | 26 | 6 | 0.0002 | 1644 |
| TFPDLESEFQA | 26 | = | | 1645 |
| TLGEVPAA | 49 | • | | 1646 |
| TMNYPLWSQSY | 74 | = | | 1647 |
| TSYVKVLH | 281 | 8 | | 1648 |
| TSYVKVLHH | 281 | 6 | 0.5900 | 1649 |
| VAELVHFLLLK | 113 | = | -0.0002 | 1650 |
| VDPIGHLY | 691 | 8 | | 1651 |
| VDPIGHLYIF | 691 | 10 | 0.0003 | 1652 |
| VDPIGHLYIFA | 691 | = | | 1653 |
| VGNWOYFF | 140 | ∞ | - | 1654 |
| VLEVFEGR | 227 | 8 | 0.0016 | 1655 |
| VTLGEVPA | 48 | ∞ | | 1656 |
| VTLGEVPAA | 48 | 6 | 0.0003 | 1657 |
| VVGNWOYF | 139 | • | | 1658 |
| VVGNWQYFF | 139 | 6 | 0.0022 | 1659 |
| WGPRALVETSY | 273 | = | | 1660 |
| YFFPVIFSK | 145 | σ: | 0.0020 | 1991 |
| YFFVIFSKA | 7. 7. | 2.5 | 5000.0 | 1663 |
| VVKVI HHMVK | 283 | 01 | 0.0020 | 1664 |
| | } | • | | |

| Ĵ | Table XVII A Mage 2 All Motif Peptides with Binding Data |
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| | | TAILEY A CALL LANGE A PRINCES THEIR PRINCES | 1112 Zava | |
|-------------|----------|---|-----------|------------|
| Sequence | Position | No. of Amino Acids | A*1101 | SEQ ID NO. |
| AADSPSPPH | 55 | 6 | 6000:0 | 1665 |
| ACYEFLWGPR | 267 | 01 | 0.0035 | 1666 |
| ADSPSPPH | 56 | : ∞ | | 1667 |
| AIEGDCAPEEK | 210 | = | 0.0007 | 1668 |
| AISRKMVELVH | 801 | = | | 1669 |
| ALIETSYVK | 772 | 6 | 0.1900 | 1670 |
| ASSFSTTINY | 89 | 01 | 0.0260 | 1671 |
| DFFPVIFSK | 145 | . 6 | 0.0022 | 1672 |
| DLVQENYLEY | 249 | 10 | | 1673 |
| DLVÕENYLEYR | 249 | = | 0.0018 | 1674 |
| DSVFAHPR | 236 | : ∞ | 0.0005 | 1675 |
| DSVFAHPRK | 236 | 6 | 0.0025 | 1676 |
| EDSVFAHPR | 235 | 6 | | 1677 |
| EDSVFAHPRK | 235 | 10 | | 1678 |
| EFQAAISR | 104 | ∞ | | 1679 |
| EFQAAISRK | 104 | 6 | 0.0002 | 1680 |
| EGDCAPEEK | 212 | 6 | 0.0001 | 1891 |
| EGREDSVFAH | 232 | 01 | | 1682 |
| ELSMLEVFEGR | 224 | | 0.0008 | 1683 |
| ELVHFLLLK | 115 | : 6 | 0.0011 | 1684 |
| ELVHFLLLKY | 115 | 10 | 0.0003 | 1685 |
| ELVHFLLLKYR | 115 | = | 0.0031 | 1686 |
| EMLESVLR | 134 | ∵ ∞0 | -0.0003 | 1687 |
| ESEFOAAISR | 102 | 0 | 0.0002 | 1688 |
| ESEFQAAISRK | 102 | = | 0.0004 | 1689 |
| ETSYVKVLH | 280 | 6 | | 1690 |
| ETSYVKVLHH | 280 | 01 | | 1691 |
| EVVEVVPISH | 165 | 01 | 0.0002 | 1692 |
| EVVPISHLY | 168 | 6 | 0.0002 | 1693 |
| FFPVIFSK | 146 | ∞ | | 1694 |
| FLLLKYRAR | 611 | 6 | | 1695 |
| FSTTINYTLWR | 7.1 | = | 0.0170 | 1696 |
| GASSFSTTINY | 29 | = | | 1691 |
| GDCAPEEK | 213 | ∞ | | 8691 |
| GDNOVMPK | 161 | ∞ | | 6691 |
| GGEPHISY | 294 | ∞ | 1 1 1 | 1700 |
| GLLGDNQVMPK | 188 | = | 0.0047 | 1201 |
| GSSNQEEEGPR | 98 | = | -0.0002 | 1702 |
| HCKPEEGLEAR | 6 | = | | 1703 |
| HFLLLKYR | 118 | ∞ | | 1704 |
| HFLLLKYRAR | 118 | 10 | 0.0002 | . 1705 |
| HISYPPLH | 298 | ∞ : | • | 1706 |
| HISYPPLHER | 298 | 01 | 0.0018 | 1707 |
| HTLKIGGEPH | 289 | 01 | | 1708 |
| IFSKASEY | 150 | ∞ (| | 60/1 |
| IGGEPHISY | 567 | 5 | | 21/1 |

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| 1711 | 1712 | 1713 | 1714 | 1715 | 1715 | 1716 | 1717 | 1717 | 1717 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 | 1727 |

| 1 | • | A' | 67 | VIIA |
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| C | | | | Table XVII |

SEQ ID NO.

| | | Table XVIIA Mage 2 All Motif Peptides with Binding Data | <u>tta</u> | |
|--|------------|---|------------|---|
| Sequence | Position | No. of Amino Acids | A*110} | S |
| ILVTCLGLSY | 177 | Õl | 0.0002 | |
| ISRKMVELVH ISYPPLHER | 109 299 | 01 6 | 0.0002 | |
| KAEMLESVLR | 132 | 01 | 0.000 | |
| KIGGEPHISY | 292 | 0. | 90 | |
| LCDNOVMPK | 787 180 | × | 0.0100 | |
| LIETSYVK | 278 | ~ ∞ | 0.0027 | |
| LIETSYVKVLH | 278 | = | | |
| LLGDNQVMPK | 681 | 01 0 | 0.0014 | |
| LLMODLVOENY | 245 | • = | t000:01 | |
| LMODLVQENY | 246 | : 01 | | |
| LSMLEVFEGR | 225 | 01 | 0.0001 | |
| LVHFLLLK | 9 7 7 | ∞ ດ | 0.1500 | |
| LVHFLLLKYR | 911 | 0.0 | 0.0022 | |
| LVQENYLEY | 250 | ? 6 | | |
| LVQENYLEYR | 250 | 01 | 0.0089 | |
| LYTCLGLSY | 178 777 | 600 | -0 0004 | |
| MVELVHFLLLK | 113 | ° = | 0.0120 | |
| PAADSPSPPH | 54 | 01 | | |
| PACYEFLWGPR | 266 | = • | -0.0002 | |
| PLEORSOH | 797 7 | ∞ ∞ | | |
| PLEQRSQHCK | 7 | .00 | 0.0002 | |
| PLHERALR DVIESVASEV | 303 | ∞ ⊆ | -0.0004 | |
| ODFFPVIFSK | 144 | 2 2 | 0.0083 | |
| ODLVQENY | 248 | .∞: | | |
| QDLVQENYLEY | 248 | <u></u> <u>-</u> | | |
| RALIETSY | 276 | 2 ∞ | | |
| RALIETSYVK | 276 | 01 | 0.0750 | |
| RAREPVTK | 125 05 | ∞ ∘ | -0.0003 | |
| SESTINATION OF SECTION | 9,6 | • • | 0 0220 | |
| SNQEEEGPR | 88 | v 0v | 0.0001 | |
| SSFSTTINY | 69 5 | 6 | 6000 | |
| SSNQEEEGPR STTINYTI WR | 87 | 2 2 | 0.0010 | |
| SVFAHPRK | 237 | 2 ∞ - | 0.0810 | |
| TINYTLWR | 74 290 | ∞ o₁ | 0.0550 | |
| TSYVKVLH | 281 | . ∞ | | |
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| L | | | Table XVI |

| - | | Lable AVIL B. Lable AVIL B. Mage 3 All Motif Peptides with Binding Data | g Data | |
|----------------------------|----------|---|---|------------|
| Sequence | Position | No. of Amino Acids | A*1101 | SEQ ID NO. |
| ACYEFLWGPR | 267 | 01 | 0.0035 | 1767 |
| ALSRKVAELVH | 801 | = | | 1768 |
| ALVETSYVK | 277 | 6 | 0.1700 | 1769 |
| ASSLPTTMNY | 89 | 01 | 0.0330 | 1770 |
| ATCLGLSY | 179 | ∞ ₁ | *************************************** | 1771 |
| DSILGDPK | 236 | ∞ ₁ | -0.0003 | 2//1 |
| DSILGOPKK | 236 | 6 | -0.0002 | 17/3 |
| EDSILGDPK | 235 | 6 | 0.0002 | 1774 |
| EDSILGDPKK | 235 | 10 | 0.0002 | 1775 |
| EFQAALSR | 104 | ∞ | | 1776 |
| EFQAALSRK | 401 | 6 | 0.0001 | 1771 |
| EGDCAPEEK | 212 | 6 | 0.0001 | 1778 |
| ELMEVDPIGH | 165 | 10 | 0.0002 | 1779 |
| ELSVLEVFEGR | 224 | = | 0.0023 | 1780 |
| EL VHELLIK | 115 | : o | 0.0011 | 1781 |
| EI VHFI I I KY | 115 | 01 | 0 0003 | 1782 |
| ELVIELLIVO | . = | ? - | 0.0031 | 1783 |
| CLVHILLININ | 2 2 | | 1600.0 | 1784 |
| ESELVALSA ESELOA AL SBV | 20.5 | ⊇: | 20000 | 1206 |
| ESEFQAALSKA | 707 | = < | ±000.0 | 1785 |
| EISTVRVLH | 787 | ~ ; | | 09/1 |
| EISYVKVLHH | 780 | 2 | | /8/1 |
| EVDPIGHLY | 891 | 6 | 0.0009 | 1788 |
| FATCLGLSY | 178 | 6 | 0.0004 | 68/1 |
| FFPVIFSK | 146 | 8 | | 06/1 |
| FLLLKYRAR | 611 | 6 | | 16/1 |
| FVQENYLEY | 250 | 6 | | 1792 |
| FVQENYLEYR | 250 | 01 | 0.0012 | 1793 |
| GASSLPTTMNY | 29 | = | | 1794 |
| GDCAPEEK | 213 | 80 | | 1795 |
| GDNQIMPK | 161 | ∞ | | 1796 |
| GDPKKLLTQH | 240 | 10 | 0.0002 | 1797 |
| GGPHISYPPLH | 295 | = | | 1798 |
| GLLGDNQIMPK | 188 | = | 0.0570 | 1799 |
| GSVVGNWQY | 137 | 6 | | 1800 |
| HCKPEEGLEAR | 6 | = | | 1801 |
| HFLLLKYR | 118 | ∞ | | 1802 |
| HFLLLKYRAR | 118 | 10 | 0.0002 | 1803 |
| HFVQENYLEY | 249 | 01 | | 1804 |
| HFVQENYLEYR | 249 | = | | 1805 |
| HISYPPLH | 298 | ∞ | | 1806 |
| HMVKISGGPH | 289 | 10 | | 1807 |
| IFATCLGLSY | 171 | 01 | 0.0004 | 1808 |
| IIVLAIIAR | 203 | 6 | 0.0011 | 1.809 |
| ISGGPHISY | 293 | 6 | 0.0002 | 1810 |
| IVLAIIAR | 204 | ∞ | 0.0037 | 1811 |
| KISGGPHISY | 292 | 01 | | 1812 |
| KVLHHMVK | 285 | ∞ | 0.0190 | 1813 |

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| // | Table 7 |
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| WIRK 190 ATIIOI ATIIOI MARKAYY 150 9 11 MANAYY 129 10 6,0012 MARKAY 229 10 6,0012 MARKAY 215 10 6,0012 MARKAY 215 10 6,0012 MARKAY 215 11 6,0002 MARKAY 125 11 0,0002 MORINY 156 9 0,0002 MORINY 278 11 0,0002 < | Sequence LGDNQIMPK LGDPKKLLTQH LGSVGNWQY LLIVLAIIAR LLIVLAIIAR LLITQHFVQENY LLITQHFVQENY LLMEVDPIGH CREVDPIGH CREVDFIGH | Position 190 239 | No. of Amino Acids | A*1101 | SEQ ID NO. |
|---|---|------------------|-----------------------|---------|------------|
| H 199 9 9 00012 1359 19 9 9 10 00012 1359 19 9 10 10 00012 1359 19 10 10 00012 1359 19 10 10 00012 1359 19 10 10 00012 1359 10 10 10 00014 1350 10 10 10 10 10 10 10 10 10 10 10 10 10 | CDDNQIMPK CDPKKLLTQH CSVVGNWQY LIJIVALIAR LLINVLAIIAR LLINVLAIIAR LLIKYRAR LLKYRAR LLTQHFVQENY LMEVDPIGH LMEVDPIGH | 190 | | | |
| HH 1239 Y 245 190 190 190 190 190 190 190 190 | GDEKKLLTQH GSVVGNWQY LIVLAIIAR LIOLAIIAR LLIVLAIIAR LLIVLAIIAR LLTQHFVQENY MEVDPIGHLY SRKVAFI VH | 239 | | | 7 101 |
| Y 252 Y 252 X 253 X 252 X 252 X 252 X 252 X 253 X | GSVGNWQY GSVGNWQY LIGDNQIMPK LIIVLAIIAR LLIVLAIIAR LLTQHFVQENY MEVDPIGHL SRKVAFI VH | 6C7 | ^ : | | 1014 |
| Y | LUSYVORWQY LIVAIIAR LIIVLAIIAR LLIVLAIIAR LLIKYRAR LLTQHFVQENY MEVDPIGH MEVDPIGHLY | | = : | | 5181 |
| Y 122 Y 124 Y 125 Y 126 Y 126 Y 126 Y 126 Y 126 Y 126 Y 127 H 278 H | LGDNQIMPK LLIVLAIIAR LLIKYRAR LTQHFVQENY MEVDPIGH MEVDPIGHLY SRXVAFI VH | 95- 202 | 2 5 | 0.0012 | 2 5 |
| γ γ 120 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | LLIVLAINAR LLIKYRAIR LTQHFVQENY MEVDPIGH MEVDPIGHLY | 707 | 2: | 0.002 | /181 |
| γ γ 120 γ γ 166 γ γ 175 γ γ γ 175 γ γ 175 | LLKYRAR LLKYRAR LTQHFVQENY MEVDPIGH MEVDPIGHLY | 189 | 2: | 0.000 | 8181 |
| Y 1665 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | LLN I NAN LTQHFVQENY MEVDPIGH MEVDPIGHLY SPKVAFI VH | 107 | = « | 0.0038 | 6181 |
| Y 166 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | .LIÇHFVÇENY .MEVDPIGH .MEVDPIGHLY SRKVAFI VH | 071 | ∞ ; | -0.0004 | 1820 |
| Y 166 1 105 1 225 2 245 1 10 000000 2 25 2 25 3 20 4 116 5 20 6 20 7 7 75 7 7 75 7 8 8 8 000000 7 8 7 74 7 8 8 8 0000000 8 8 00000000000000000 | .MEVDPIGH .MEVDPIGHL.Y SRKVAFI VH | 242 | = | • | 1821 |
| 1 105 10 10 10 10 10 10 | MEVDPIGHLY SRKVAFI VH | 99 | • | 0.0001 | 1822 |
| 110 00000 226 10 000000 228 8 8 000014 1116 9 9 00001 220 113 111 220 00000 230 111 000000 24 111 000000 25 10100 26 20 111 000000 27 2 100000 28 8 000000 29 20 000000 20 0000000000000000000000000 | CREVAEIVH | 991 | = | | 1823 |
| H 223 10 00030 H 278 8 11 00002 Z 28 8 00002 QY 135 11 00002 QY 135 11 00002 QY 250 9 0 00002 Z 2 8 8 00002 Z 2 8 8 00002 Z 303 8 8 00002 Z 2 8 8 00002 Z 2 8 8 00002 Z 2 8 8 00002 Z 303 8 8 00002 Z 2 8 8 00002 Z 2 8 8 00002 Z 303 8 8 00002 Z 2 8 8 00002 Z 303 8 8 00002 Z 4 11 11 11 11 11 11 11 11 11 11 11 11 1 | | 601 | 01 | 0.0002 | 1824 |
| 246 H 1278 H 1278 116 116 116 116 9 110 0,0002 0,0014 120 0,0014 120 0,0014 120 0,0014 120 0,0010 0,0010 0,0010 0,0010 0,0002 0,0002 0,0002 0,0002 0,0002 0,0002 0,0002 0,0002 0,0002 0,0002 0,0002 0,0003 0,0004 0,0003 0,0003 0,0003 0,0003 0,0003 0,0003 0,0003 0,0003 0,0003 | SVLEVFEGR | 225 | 10 | 0.0030 | 1825 |
| H 278 8 0.0014 116 8 8 11 116 8 8 11 116 9 0.1500 117 75 110 117 110 QY 77 75 110 118 111 XY 77 75 110 119 0.0002 120 8 8 0.0003 120 0.1100 121 8 8 0.0003 122 8 8 0.0003 123 8 8 0.0003 124 8 8 0.0003 125 8 8 8 0.0003 126 9 9 0.1400 127 14 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | TQHFVQENY | 246 | 10 | 0.0002 | 1826 |
| H 118 8 11 0.1500 QY 116 9 0.0100 QY 1280 0.0100 QY 1280 11 0.0002 RR 286 10 0.0002 RR 286 10 0.0002 RR 287 8 8 0.0002 RR 288 8 0.0002 RR 288 8 0.0002 RR 113 11 11 11 11 11 11 11 11 11 11 11 11 | VETSYVK | 278 | • | 0.0014 | 1827 |
| 116 9 0.1500 116 135 116 100 0.00022 125 10 0.0002 126 10 0.0002 126 11 0.0002 127 128 8 0.0003 128 128 8 0.0003 128 138 8 0.0003 128 138 8 0.0001 128 138 8 0.0001 128 138 8 0.0001 129 138 8 0.0001 140 141 141 141 141 142 143 150 150 150 150 | VETSYVKVLH | 278 | = | | 1828 |
| 9 0.0100 116 10 0.0002 17 20 10 0.0002 18 20 0.0002 2 2 8 8 0.0002 2 2 8 8 0.0002 2 2 10 0.0002 3 3 3 8 0.0002 3 3 4 11 0.0001 5 4 11 0.0001 5 5 7 7 8 8 0.0006 5 6 9 9 0.1400 5 7 7 8 8 0.0005 5 8 0.0005 5 7 8 8 0.0005 5 8 0.0005 5 8 0.0005 5 8 0.0005 | VHFLLLK | 116 | : oc | 0.1500 | 1829 |
| Oy 116 10 00002 NR 250 11 0 00002 RR 250 8 8 000002 2 2 8 8 000002 2 3 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 2 2 8 8 000002 3 3 3 8 8 000002 5 4 11 1 11 11 11 11 11 11 11 11 11 11 11 | VHFLLLKY | 116 | · • | 00100 | 1810 |
| QY 135 11 0 00002 250 250 9 9 0 00002 250 250 250 250 250 250 250 250 | VHFLLLKYR | 911 | \ <u>C</u> | 0.000 | 1831 |
| 75 75 76 77 77 77 77 77 77 77 77 77 77 77 77 | AOMNUANU II | 135 | 2 - | 7700:0 | 1631 |
| RR 256 256 267 268 88 276 88 276 88 80 276 88 88 90 90 90 90 90 90 90 90 90 90 | Neos Sign | 56 | - 5 | 2000 0 | 1632 |
| NR 256 11 - 0.0002 2 | TO SECURITION OF THE PROPERTY | Coc | ≥ < | 0.000 | 1833 |
| 20002 2 | ACVEEL WORD | 067 | ^ : | 0.0002 | 1634 |
| 2 8 8 0.0002 2 303 303 8 8 -0.0003 226 10 276 8 8 0.1100 277 8 8 0.0012 278 8 0.0012 279 8 8 0.0012 270 8 8 0.0002 271 9 9 0.1400 271 11 0.0005 272 8 8 0.0005 273 11 0.0005 | ACTER OTA | 200 | = • | -0.002 | 1835 |
| 2 1 8 0,0002 303 8 8 -0,0003 256 10 8 8 -0,0003 276 10 8 8 0,01100 277 8 8 0,0012 270 8 8 0,0012 271 8 8 0,0012 272 281 8 8 8 281 8 8 8 281 8 8 0,0006 273 111 0,0011 174 113 111 K 273 111 175 117 | USDPACY | 797 | × • | | 1836 |
| 2 10 0,0002 2,0003 3,03 8 8 0,0003 2,0003 3, | LECKSCH | 7 | ~ | | 1837 |
| 2Y 266 10 10 100 | LEQRSQHCK | 2 | 01 | 0.0002 | 1838 |
| 7Y 260 10 10 276 8 8 6.1100 2.1100 2.276 10 2.2776 10 2.2776 10 2.2776 237 8 8 6.0012 237 8 8 6.0012 2276 281 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | LHEWVLR | 303 | ∞ | -0.0003 | 1839 |
| 125 8 125 8 125 8 294 8 237 8 237 8 237 8 70 8 69 9 69 9 70 9 69 9 69 0.1400 7 138 8 0.0066 11 11 169 8 169 8 170 11 170 11 11 0.0005 11 0.0270 | VPGSDPACY | 260 | 01 | | 1840 |
| 125 8 0.1100 294 8 0.0003 237 8 0.0012 70 8 0.0012 69 9 0.1400 62 9 0.1400 138 8 0.1400 4 281 8 0.0066 11 11 0.0011 169 8 0.0005 157 273 11 0.0270 SY 176 11 0.0270 | ALVETSY | 276 | 80 | | 1841 |
| 294 8 -0.0003 294 8 8 -0.0003 70 8 8 0.0012 70 8 8 0.0012 226 9 9 0.1400 138 8 8 0.1400 4 281 8 8 0.0066 14 281 9 0.0011 169 8 0.0001 15Y 273 11 5SY 176 111 | ALVETSYVK | 276 | 01 | 0.1100 | 1842 |
| 294 8 0.0012 70 8 8 0.0012 71 8 8 0.0012 72 226 9 9 0.1400 73 138 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | AREPVTK | 125 | ∞ | -0.0003 | 1843 |
| 237 8 0.0012 70 8 8 0.0012 71 28 9 9 0.1400 72 226 9 9 0.1400 73 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | GGPHISY | 294 | ∞ | | . 1844 |
| 70 8 8 9 0.1400 226 9 9 0.1400 3138 8 8 8 0.0066 4 281 8 8 0.0066 14 281 9 0.0011 157 273 8 0.0005 158 273 11 58 5.0005 | ILGDPKK | 237 | • | 0.0012 | 1845 |
| 69 9 0.1400 138 8 8 0.1400 138 8 8 0.1400 4 281 8 8 0.0066 14 281 9 0.0066 15 227 8 8 0.0005 15 273 11 11 0.0270 | LPTTMNY | 70 | - ∞ | | 1846 |
| 226 9 0.1400 138 8 8 0.1400 4 281 8 8 0.0066 1 281 9 0.0066 1 13 11 11 0.0011 157 273 8 0.0005 158 273 11 0.0270 | SLPTTMNY | 69 | . 6 | | 1847 |
| Y 74 138 8 8 8 74 74 11 11 11 11 11 11 11 11 11 11 11 11 11 | VLEVFEGR | 226 | . 6 | 0.1400 | 1848 |
| Y 74 11 281 8 0,0066 113 111 0,0011 169 8 8 0,0005 Y 273 8 0,0005 11 145 9 0,0270 | VVGNWQY | 138 | . 00 | | 1849 |
| 281 8 0.0066 281 9 0.0066 113 111 0.0011 169 8 0.0005 7 227 8 111 0.0270 176 111 111 | MNYPLWSQSY | 74 | = | | 1850 |
| 281 9 0.0066 113 111 0.0011 169 8 0.0005 7 273 111 0.0270 | SYVKVLH | 281 | ∵∞ | | 1881 |
| 113 | SYVKVLHH | 281 | 6 | 0.0066 | 1852 |
| 169 8 0.0005 1 | AELVHFLLLK | 113 | = | 0.0011 | 1853 |
| Y 227 8 0.0005 1 273 11 11 0.0270 1 176 11 11 | DPIGHLY | 169 | 8 | | 1854 |
| Y 273 II 0.0270 I I I 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | LEVFEGR | 227 | 80 | 0.0005 | 1855 |
| SY 176 11 6 11 6 11 6 11 11 11 11 11 11 11 11 | /GPRALVETSY | 273 | = | | 1856 |
| 11 11 11 11 11 11 11 11 11 11 11 11 11 | FFPVIFSK | 145 | 6 | 0.0270 | 1857 |
| | YIFATCLGLSY | 176 | = | | 1858 |

| | | THE STATE OF THE PRINCES WITH | Dinamic Party | |
|-------------|----------|-------------------------------|---------------|------------|
| Sequence | Position | No. of | A*240! | SEQ ID NO. |
| | | Amino Acids | | |
| CYEFLWGPRAL | 268 | | 0.0004 | 1860 |
| EFLWGPRAL | 270 | : 6 | 90000 | 1861 |
| EFLWGPRALI | 270 | 01 | 0.0097 | 1862 |
| EYLOLVFGI | 156 | 6 | 3.5000 | 1863 |
| IFSKASEYL | 150 | 6 | 0.0230 | 1864 |
| IFSKASEYLOL | 150 | | 0.0950 | 1865 |
| IWEELSML | 221 | ∞ | 0.0007 | 1866 |
| IWEELSMLEVF | 221 | = | 0.0170 | 1867 |
| KMVELVHF | 112 | • | 0.0005 | 1868 |
| KMVELVHFL | 112 | 6 | | 1869 |
| KMVELVHFLL | 112 | 10 | | 1870 |
| KMVELVHFLLL | 112 | = | | 181 |
| LMODLVOENYL | 246 | _ | | 1872 |
| LWĞPRALİ | 272 | & | 0.1200 | 1873 |
| LYILVTCL | 175 | 8 | 9800'0 | 1874 |
| LYILVTCLGL | 175 | 01 | 0.0140 | 1875 |
| MFPDLESEF | 26 | 6 | 0.0140 | 1876 |
| RMFPDLESEF | 96 | 01 | 0.0016 | 1877 |
| SFSTTINYTL | 70 | 01 | 0.0150 | 1878 |
| SFSTTINYTLW | 70 | = | 0.0280 | 1879 |
| SYPPLHERAL | 300 | 01 | 0.0003 | 1880 |
| SYVKVLHHTL | 282 | 01 | 0.1600 | 1881 |
| VFAHPRKL | 238 | • | 0.0005 | 1882 |
| VEAHPRKLL | 238 | . 6 | 90000 | 1883 |
| VFEGREDSVF | 230 | 01 | 0.0004 | 1884 |
| VMPKTGLL | 195 | ∵∞ | -0.0004 | 1885 |
| VMPKTGLLI | 195 | 6 | 0.2300 | 1886 |
| VMPKTGLLII | 195 | 01 | 0.0580 | 1887 |
| | | | | |

Table XVIII A
Mage 2 A24 Motif Peptides with Binding Data

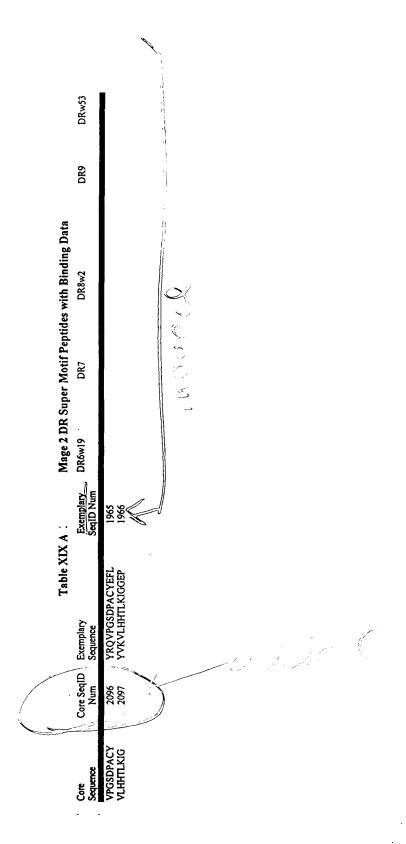
| | | Table XVIII B | Mage 3 A24 Motif Pentides with Binding Data |
|------------|-------------|---------------|---|
| <i>C</i> . | <u></u> | Table | Mage 3 A 24 Motif Per |

| | | Mage 3 A24 Motif Peptides with B | inding Data | |
|-------------|----------|----------------------------------|-------------|------------|
| Sequence | Position | No. of | A*2401 | SEQ ID NO. |
| | | Amino Acids | | |
| CYEFLWGPRAL | 268 | = | 0.0004 | 1888 |
| EFLWGPRAL | 270 | 6 | 0.0006 | 1889 |
| EMLGSVVGNW | 134 | 10 | 0.0017 | 1890 |
| HFVQENYL | 249 | ∵∞ | -0.0004 | 1881 |
| HMVKISGGPHI | 289 | = | | 1892 |
| IFATCLGL | 177 | ∞ | 0.0120 | 1893 |
| IFSKASSSL | 150 | 6 | 0.0160 | 1894 |
| IFSKASSSLQL | 150 | = | 0.0910 | 1895 |
| IMPKAGLL | 195 | ∞ | | 9681 |
| IMPKAGLLI | 195 | 6 | 0.4200 | 1897 |
| IMPKAGLLII | 195 | 10 | 0.0500 | 1898 |
| IWEELSVL | 221 | • | -0.0004 | 1899 |
| IWEELSVLEVF | 221 | = | 0.0260 | 1900 |
| LMEVDPIGHL | 166 | 10 | | 1061 |
| LYIFATCL | 175 | ∞ | 0.0140 | 1902 |
| LYIFATCLGL | 175 | 01 | 0.0480 | 1903 |
| NWQYFFPVI | 142 | 6 | 0.5300 | 1904 |
| NWQYFFPVIF | 142 | 01 | 0.0170 | 1905 |
| QYFFPVIF | 144 | ∞ | 0.1200 | 9061 |
| SYDGLLGDNQI | 185 | = | 0.0026 | 1907 |
| SYPPLHEW | 300 | ∞ | 0.0420 | 1908 |
| SYPPLHEWVL | 300 | 10 | 0.5900 | 1909 |
| TFPDLESEF | 97 | 6 | 0.0049 | 0161 |
| VFEGREDSI | 230 | 6 | -0.0004 | 1161 |
| VFEGREDSIL | 230 | 10 | -0.0005 | 1912 |
| | | | | |

| | DR5w12 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | ٠. | | | | | | | | |
|--|------------------------|-----------------|-------------------|-----------------|-----------------|------------------|-----------------|-----------------|---------------------------------------|-----------------|-----------------|-----------------|----------------|-----------------|-----------------|----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|---------------------------|-----------------|------------------------------------|-----------------|-----------------|--------------------|-----------------|-----------------|---------|-----------------|-------------------|--|-----------------|-----------------------------------|--------------------|
| | DR5w11 | | | | | | | 0.0270 | | | | -0.0005 | | | | | | | -0.0005 | | | | | | | | | | | | | | | | | | | | | |
| | DR4w15 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| g Data | DR4w4 | -0.0032 | 0.003 | -0.0032 | | | -0.0032 | 0.1600 | | | | 0.0070 | -0.0032 | | | | | | 0.0370 | -0.0032 | 0.0051 | 0.0120 | | | | -0.0032 | | | | | | | | -0.0032 | 700.0 | | | | | |
| ith Bindin | DR3 | | 0.1400 | 0.0130 | | | | 0.0113 | | | | 0.0036 | | | | 0.0660 | | | 0.0025 | | | | | | | | | | | 0.0072 | | 0.1500 | | | | | | | | |
| Mage 2 DR Super Motif Peptides with Binding Data | DR2w2B2 | | | | | | • | 1.0000 | | | | 0.000 | | | | | | | -0.0022 | | | | | | | | | | | | | | | | | | | | | |
| per Motif | DR2wB1 | | | | | | | 0.0620 | | | | 0.0046 | | | | | | | 0.0037 | | | | | | | | | | | | | | | | | | | | | |
| 2 DR Su | DRI | 0.0330 | \$000 | 9 | | | -0.0003 | 1.2000 | | | | 0.0084 | 0.0100 | | | | | | 0.0120 | -0.0003 | 0.0120 | 0.0086 | | | 0 | 0.0019 | | | | | | | | 0 0008 | | | | | | |
| Mage | Position | 24 | 2 2 | 28 | 22 | <u> </u> | 382 | 돌 9 | 4 4 | 5 6 | Z | <u>5</u> 6 | 707 | 176 | 9 5 | 200 | 175 | 134 | 8 | 3 23 | 8 | <u> </u> | <u>3 8</u> | 47 | 21 5 | 2 2 | 6 | 108 | 250 | 191 | 8/7 | 242 | 175 | ‡ ≅ | 116 | <u>8</u> : | <u> </u> | 224 | 178 | 303 |
| Table XIX A | Exemplary SeqID Num | 1913 | 1914 | 9161 | 1917 | 8161 | 1920 | 1921 | 2261 | 192 | 1925 | 1926 | 1928 | 1929 | 1930 | 1931 | 1833 | 1934 | 1935 | 1937 | 1938 | 1939 | 1940 | 1942 | 1943 | 1945 | 1946 | 1947 | 1949 | 1950 | 1953 | 1953 | 1954 | 1956 | 1957 | 1958 | 1960 | 1961 | 1967 | 2 <mark>6</mark> 2 |
| Table | Exemplary Sequence | ALGLVGAOAPATEEO | DGI I GNADVMPKTGI | EEKIWEELSMLEVFE | EFLWGPRALIETSYV | ENVI FVROVPGSDPA | EPHISYPPLHERALR | ESEFOAAISRKMVEL | EVILGEVPANDSPSP FEDVIFCK A SEVI OI | FPVIFSKASEYLOLV | GEALGLYGAQAPATE | GIEVVEVVPISHLYI | HELLKYRAREPVTK | HLYILVTCLGLSYDG | IEVVEVVPISHLYIL | IIAIEGIAAFEENW | ISHLYILVTCLGLSY | KAEMLESVLRNCODF | KTGLLIIVLAIIAIE | LGLVGAOAPATEEOO | LIIVLAIIAIEGDCA | LLIIVLAIIAIEGDC | LOLVFGIEVVEVVPI | LVEVTLGEVPAADSP | MVELVHFLLLKYRAR | PRKLLMODLVOENYL | PRMFPDLESEFOAAI | OAAISKKMVELVHFL ODFFPVIFSKASFYI | ODLVOENYLEYROVP | OLVFGIEVVEVVPIS | REPUTKA EMILESVI.R | RKLLMODLVOENYLE | SHLYILVTCLGLSYD | | VELVHFLLLKYRARE | VEVVPISHL YIL VTC | VVPISHLYILVTCLG | WEELSMLEVFEGRED | YELWGPKALIEISY YILVTCLGLSYDGLL | YPPLHERALREGEE- |
| ` | Core Seq1D Num | 2044 | 2045 2045 | 2047 | 2048 | 2049 | 2051 | 2052 | 2053 | 2055 | 2056 | 2057 | 2059 | 2060 | 2061 | 2062 | 2064 | 2065 | 2066 | 706 7068 | 2069 | 2070 | 2072 | 2073 | 2074 | 2076 | 2077 | 2078 | 2080 | 2081 | 2083 | 2084 | 2085 | 2087 | 2088 | 2089 | 763 763 763 763 763 763 763 763 763 763 | 2092 | 2093 2094 | 2095 |
| | Core Sequence | LVGAQAPAT | LSTDGCLGD | IWEELSMLE | WGPRALIET | FYROVPGS | ISYPPLHER | FOAAISRKM | VIESKASEV | IFSKASEYL | LGLVGAOAP | VVEVVPISH | LLKYRAREP | ILVTCLGLS | VEWPISHL | IAMARE | LYILVICLG | MLESVLRNC | LLIMLAII | VGAOAPATE | VLANAEG | VLAIIAIE | VFGIEVVEV | VTLGEVPAA | LVHFLLLKY | LLMODLVOE | FPDLESEFO | ISKKMVELV FPVIFSK AS | VOENYLEYR | FGIEVVEVV | VTKAEMLES | LMODLVOEN | YILVTCLGL | LIMAIA | VHFLLLKYR | VPISHLYIL | IEVVEVVPI ISHLYTLVT | LSMLEVFEG | LWGPKALIE | LHERALREG |

| Core SeqID Sequence Sequence Num Sequence Num Sequence Sequence 2044 ALGLVGAQAPATEEQ 2045 CLGLSYDGLLGDNQY 2045 CLGLSYDGLLGDNQY 2045 EKIWEELSMLEVFE 2049 EKIWEELSMLEVFE 2049 EKIWEELSMLEVFE 2049 EKIWEELSMLEVFE 2049 EKIWEELSMLEVFE 2050 ENYLEYPQPEANLR 2051 EPHISYPPLHERALR 2052 EPHISYPPLHERALR 2053 EPHISYPPLHERALR 2054 EFPVIFSKASEYLQL 2054 EPHISYPPLHERALR 2055 EPHISYPPLHERALR 2055 EPHISYPPLHERALR 2055 EPHISYPPLHERALR 2055 EPHISKASEYLQL 2056 EPHISYPPLHERALR 2056 EHVICHOLOGYPATE 2066 ENYLEYPRENCOPF 2067 ENTLANDINATIOLOGYPANDS 2073 ENYLEYPRENCOPF 2073 ENYLEYPRENCOPF 2074 ENYLENDOLVGENYL 2075 ENYLEYPRENCOPF 2076 2076 ENYLEYPRENCOPF 2076 ENYLEYPRENCOPF 2076 2076 ENYLEYPRENCOPF 2076 2076 ENYLEYPRENCOPF 2076 | One SeqUD Exempley Exempley Exempley DR6W19 DR5 DR5 2004 A.GLYGOQAPATER 913 -0.0011 -0.0011 DR5 DR5 2004 A.GLYGOQAPATER 913 -0.0011 -0.0011 DR5 DR5 <th></th> <th>,</th> <th>Table XIX A</th> <th>XA</th> <th>Mage 2 DR Sup</th> <th>er Motif Peptid</th> <th>Mage 2 DR Super Motif Peptides with Binding Data</th> <th></th> <th></th> | | , | Table XIX A | XA | Mage 2 DR Sup | er Motif Peptid | Mage 2 DR Super Motif Peptides with Binding Data | | |
|---|--|---------------|-------------------|--|------------------------|---------------|-----------------|--|-----|-------|
| 2044 ALGLVGAQAPATEEQ 1913 -0.0011 2045 CLGLSTOGLUGNQY 1914 -0.0011 2045 CLGLSTOGLUGNQY 1915 -0.0011 2047 ERIVWEELSMLEYPE 1915 -0.0011 2049 ERIVWEELSMLEYPE 1916 -0.0011 2049 ERIVWEELSMLEYPE 1917 -0.0011 2049 ERIVWEELSMLEYPE 1917 -0.0011 2049 ERIVWEELSMLEYPE 1920 -0.0011 2049 ERIVWEELSMLEYPE 1921 -0.0011 2045 ERIVACAPAIDSPR 1922 -0.0011 2045 ERIVACAPAIDSPR 1922 -0.0011 2045 ERIVACAPAIDSPR 1923 -0.0011 2045 ERIPOLACAPAIDSPR 1924 -0.0011 2045 ERIVACAPAIDSPR 1924 -0.0011 2045 ERIVACAPAIDSPR 1924 -0.0011 2045 ERIVACAPAIDSPR 1924 -0.0011 2045 ERIVACAPAIDSPR 1934 -0.0011 2045 ERIVACAPAIDSPR 1935 -0.0011 2045 ERIVACAPAIDSPR 19 | 2044 ALGLVGAQPATEEQ 1913 -0.0011 2045 CLGLSPOLLCHONQY 1914 -0.0011 2045 CLGLSPOLLCHONQY 1915 -0.0011 2047 ERIVMELSMLEYPE 1916 -0.0011 2049 ERIVMELSMLEYPE 1917 -0.0011 2049 ERIVMELSMLEYPE 1917 -0.0011 2049 ERIVMELSMLEYPE 1917 -0.0011 2049 ERIVMELSMLEYPE 1920 -0.0011 2049 ERIVMELSMLEYPE 1921 -0.0011 2049 ERIVMERSMAPE 1922 -0.0011 2049 ERIVACASTRIANT 1923 -0.0011 2049 ERIVACASTRIANT 1924 -0.0011 2049 ERIVACASTRIANT 1924 -0.0011 2049 ERIVACASTRIANT 1926 -0.0011 2049 ERIVACASTRIANT 2049 ERIVACASTR | Core Sequence | Core SeqID Num | Exemplary Sequence | Exemplary SeqID Num | DR6w19 | DR7 | DR8w2 | DR9 | DRw53 |
| 2045 CLGLSNQVAPRYTOL 2046 EKIWEELSMLEYPT 2048 EKIWEELSMLEYPT 2049 EKIWEELSMLEYPT 2050 ENYLEYROPGSDPA 1919 2051 EHFQAAISRKANEL 1921 2052 EYALGENGVAPREN 1922 2053 EYTIGENFANDSPP 1922 2054 FPWISKASEYQL 1923 2055 FPWISKASEYQL 1923 2055 FPWISKASEYQL 1924 2056 GLIINAAIARGD 1920 2057 FPWISKASEYQL 1924 2057 FPWISKASEYQL 1924 2057 GGEVGEVAPRHT 1926 2057 GGEVGEVAPRHT 1926 2057 GGEVGEVAPRHT 1926 2057 HINTOCALSYDG 1939 2057 HINTOCALSYDG 1939 2057 HINTOCALSYDG 1939 2057 HINTOCALSYDG 1939 2056 HINTOCALSYDG 1939 2057 HINTOCALSYDG 1939 2058 SELLWORDALER 1935 2058 SELLWORDALER 1935 2058 SELLWORDALER 1935 2059 VECHNELVERENED 1935 2050 VECHNELVERE | 2045 CLGLYDLCDNQV 1914 COURT 2045 CLGLYDLCDNQV 1915 COURT 2047 ERIVEELS MALEYED 1915 COURT 2049 ERIVEELS MALEYED 1915 COURT 2049 ERIVEELS MALEYED 1916 COURT 2049 ERIVEELS MALEYED 1918 COURT 2049 ERIVEELS MALEYED 1918 COURT COURT 2049 ERIVERS MARCH 1921 COURT | VGAQAPAT | 2044 | ALGLVGAQAPATEEQ | 1913 | | -0.0011 | | | |
| 2049 DOLLODIN/WINTKICL 1915 2049 ELWELSMLEYER 1916 2049 ELWELSMLEYER 1916 2049 ENTLETRY/WESDPA 1919 2049 ENTLETRY/WESDPA 1919 2040 ENTLETRY/WESDPA 1919 2040 ENTLETRY/WESDPA 1919 2040 ENTLETRY/WESDPA 1920 2045 ENTLETRY/WESDPA 1922 2045 EPH/STRALENIL 1922 2045 EPH/STRALENIL 1924 2045 EPH/STRALENIL 1924 2045 EPH/STRALENIL 1924 2045 EPH/STRALENIL 1926 2046 ELMYLANIREDD 1927 2046 ELMYLANIREDD 1927 2046 ELMYLANIREDD 1927 2046 ELMYLANIREDD 1924 2046 ELMYLENIRED 1934 2046 ELMYLANIREDD 1934 2046 ELMYLENIRENIR 1934 2046 ELMYLANIREDD 1934 2046 ELMYLENIRENIR 1934 2046 ELMYLANIREDD 1934 2046 ELMYLENIRENIRED 1934 2047 ERMYLENIRENIRED 1934 2048 ERMYLENIRENIRENIRED 1934 2048 ERWYLENIRENIRENIRENIRENIRENIRENIRENIRENIRENIR | 2040 ELLAGRAMENTOL 1915 20001 2004 ELLAGRAMENTOL 1916 2006 ELLAGRAMENTOL 1917 2006 ELLAGRAMENTOL 1917 2006 ELLAGRAMENTOL 1917 2005 ELLAGRAMENTOL 1918 2005 ERLAGRAMENTOL 1921 2005 ERLAGRAMENTOL 1921 2005 ERLAGRAMENTOL 1922 2005 ERLAGRAMENTOL 1924 2005 ERLAGRAMENTOL 1924 2005 ERLAGRAMENTOL 1926 2005 ERLAGRAMENTOL 2005 | 8 | 2045 | CLGLSYDGLLGDNQV | 1914 | | | | | |
| 2008 EFLWOPRALIETSYV 1917 2015 EFLWOPRALIETSYV 1917 2021 EPHSYROPHERALR 1920 2020 ENTLERALR 1920 2021 EPHSYROPHERALR 1920 2022 ESPEÇANIEKWHE 1921 2023 EVTIGEVPAADSSP 1922 2024 FPFVIFSKASETIQL 1922 2025 EVTIGEVPAADSSP 1922 2026 GEALGLVVAQAPATE 1925 2026 GEALGLVAGAPATE 1925 2026 GEALGLVAGAPATE 1926 2027 GIEVVEVPISHLYIL 1920 2028 HTLLKYRAREPYK 1939 2026 HTLLKYRAREPYK 1939 2026 HTLLKYRAREPYK 1939 2026 INVALIALEGOCA 1939 2027 CLGEVPAADSSPPHS 1936 2027 CLGEVPAADSSPPHS 1936 2027 LLGEVPAADSSPPHS 1936 2027 LLGEVPAADSSPPHS 1939 2027 REVERENTERARR 1931 2028 REVILLAGEVPAADS 1939 2028 REVILLAGEVPAADS 1939 2029 VECHNERALRYRAR 1935 2039 RELITYARARENTERY 1935 2039 RELITYARARENTERY 1935 2039 RELITYARARENTERY 1935 2039 RELITYARARENTERY 1935 2039 VECHNERALRYRAR 1935 2039 VECH | 2009 EKWPELSNLEYEV 1917 2009 EKWPELSNLEYEV 1918 2001 EPHSYPPLHEALR 1920 2005 ENTLERVALSSER 1920 2005 ENTLERVALSSER 1920 2005 EVTIGEVALONESP 1922 2005 EVTIGEVALONESP 1922 2005 EVTIGEVALONESP 1922 2005 GEALGLVARAPATE 1925 2006 GEALGLVARAPATE 1926 2006 GEALGLVARAPATE 1926 2006 GEALGLVARAPATE 1928 2006 GEALGLVARAPATE 1928 2006 GEALGLVARAPATE 1930 2007 GILVYARAPEPYK 1930 2006 GEALGLVARAPATE 1930 2006 GEALGLVARAPATE 1930 2007 GILVYARAPATE 1930 2008 GEALGLVARAPATE 1930 2009 HFLLIKYRAREPYK 1931 2006 GEALGLVARAPATE 1930 2006 GEALGLVARAPATE 1930 2007 GILVYARAPATE 1930 2006 GEALGLVARAPATE 1930 2007 GILVYARAPATE 1930 2006 GEALGLVARAPATE 1930 2007 GILVYARAPATE 1930 2008 CARALLINYARAPATE 1930 2009 GARGENVEVYPR 1931 2007 LURYARAPATE 1930 2007 GODVOGNYLEYRAR 1930 2007 GODVOGNYLEYRAR 1930 2007 GODVOGNYLEYRAR 1930 2008 GARGENVEVYPR 1930 2008 GARGENVEVYPR 1930 2008 GARGENVEVYPR 1930 2008 GEALGLARAPATE 1930 2008 GARGENVEVPR 1930 2008 GARGENVEVPR 1930 2009 VEGIEVVEVYRER 1930 2009 VEGIEVVERVEGE 1930 2009 VEGIEVVEVYRER 1930 2009 VEGIEVVERVEGE 1930 2009 VEGIEVREVER 1930 2009 VEGIEVREVARE 1930 2009 VEGIEVREVER 1930 2009 VEGIEVREVER 1930 2009 VEGIEVREV 1930 2009 | MLE | 2047 | EEKIWEELSMLEVFE | 1916 | | -0.0011 | | | |
| 2003 ENVIRENCIATE 1910 2015 EPHISYPELHERALR 1920 2016 EPHISYPELHERALR 1920 2016 EPHISYPELHERALR 1920 2016 EPHISYPELHERALR 1921 2017 ESPEÇAAJRRAWYEL 1921 2018 FPVIRENASETUQL 1922 2019 GEALGLVGAQAPATE 1926 2019 GEALGLVGAQAPATE 1926 2019 GEALGLVGAQAPATE 1929 2019 GEALGLVGAQAPATE 1920 2019 GEALGLVGAQAPATE 1920 2019 GEALGLVGAQAPATE 1920 2019 GEALGLVGAQAPATE 1920 2010 ILVAYRAREPYTK 1931 2010 ILVAYRAREPYTK 1931 2011 LINYCLGLSYDG 1931 2011 CANDRYELLKYNRAR 1931 2011 CANDRYELLKYNRAR 1931 2011 LINYCLGLSYDG 1931 2011 CANDRYELLKYNRAR 1931 2011 CANDRY 1931 2011 CAN | 2003 ENVIEWNING NOW 1919 2003 ENVIEWNING NOW 1919 2003 ENVIEWNING NOW 1920 2004 FEPVINSKASETIQL 1921 2005 EVILGEVRADSPS 1922 2005 FEPVINSKASETIQL 1922 2005 GEALGLVGAQAPATE 1926 2006 GEALGLVGAQAPATE 1926 2006 GEALGLVGAQAPATE 1926 2007 GEALGLVGAQAPATE 1926 2008 GEALGLVGAQAPATE 1926 2009 GEALGLVGAQAPATE 1926 2009 HTLLKYRAREPYTK 1928 2009 HTLLKYRAREPYTK 1928 2006 GLACKGAQAPATE 1930 2006 GLACKGAQAPATE 1930 2006 GLACKGAGAPATE 1930 2007 GLACKGAGAPATE 1930 2006 GLACKGAGAPATE 1930 2006 GLACKGAGAPATE 1930 2007 GAGAGAPATE 1930 2007 GAGAGAPATE 1930 2008 GLACKGAGAPATE 1930 2008 GLACKGAGAPATE 1930 2009 GAGAGAPATE 1930 2009 GAGAGAPATE 1930 2009 GAGAGAPATE 1930 2009 VEGTEVVEVPISH 2009 VEGTEVVEVPISH 2009 VEGTEVAGAPATE 1930 2009 VEGTE | LIET | 2048 | EFLWGPRALIETSYV | 1917 | | | | | |
| 2051 EPHISYPPLHERALR 1920 00067 0,00011 2052 ESEPOAASIRKWYEL 1921 00067 0,5100 2053 FPVITESKASEYLQU 1923 2054 FPVITESKASEYLQU 1924 2055 FPVITESKASEYLQU 1924 2056 GALGUAGARART 1926 0,00710 0,00011 2057 GILVEVYPRISHLYI 1928 2058 HTLLLKYRAREPYT 1928 2056 HATLLKYRAREPYT 1928 2056 HATLLKYRAREPYT 1931 2057 LINTAINIGEDCAPERKW 1931 2068 HATLLKYRAREPYT 1932 2069 HATLLKYRAREPYT 1934 2061 HATLATCLGLSYD 1932 2064 HATLLKYRAREPYT 1934 2065 LGLYGACAPATEQQ 1935 2066 LGLYGACAPATEQQ 1935 2067 LGEVPAADSPSPPHS 1936 2067 LGEVPAADSPSPPHS 1936 2067 LGEVPAADSPSPPHS 1936 2067 LGEVPAADSPSPPHS 1936 2070 LLIVAINIGEDCA 1938 2071 LLIVAINIGEDCA 1938 2072 LGEVPAADSPSPPHS 1940 2073 LVEVTLGEYVRVPH 1941 2073 LVEVTLGEYVRVPH 1941 2073 LOLVEGEYVRVPH 1941 2074 MYELVHCHTARAPT 1951 2076 GALSKAWTELNYPR 1935 2077 GALSKAWTELNYPR 1935 2078 QALSKAWTELNYPR 1935 2078 QALSKAWTELNYPR 1935 2078 QALSKAWTERNYPR 1935 2078 GALSKAWTERNYPR 1935 2078 GALSKAWTERNYPR 1935 2078 GALSKAWTELNYPR 1935 2078 GALSKAWTERNYPR 1935 2078 GALSKAWTELNYPR 1935 2078 GALSKAWTERNYPR | 2051 EPHISYPPI,HERALR 1920 -0.0011 2052 ESEFÇAAJSKWYEL 1921 0.0067 0.5100 2053 EYECKARANDENEN 1922 0.5100 2054 FFPVIESKASEVLQL 1924 0.0067 0.5100 2055 GEALGLVGAÇAPATE 1924 0.0011 0.0011 2057 GIEVLEAREPYT 1928 0.0011 0.0011 2058 HTLLKYRAEEPYT 1929 0.0011 0.0011 2059 HTLLKYRAEEPYT 1939 0.0011 0.0011 2050 HTLLKYRAEEPYTK 1939 0.0012 0.0011 2050 HTLLKYRAEEPYTK 1931 0.0011 0.0011 2050 HTALLYKYRAEEPYTK 1931 0.0011 0.0011 2051 HTALLIKYRAEEPYTK 1934 0.0011 0.0011 2052 HARLESYLRYCQDF 1934 0.0011 0.0011 2053 HARLESYLRYCQDF 1934 0.0010 0.0011 2054 HARLESYLRYCQDF 1934 | PGS 4 | 2050 | ENYLEYROVPGSDPA | 9161 | | | | | |
| 2052 ESEPQAAISRKAVEL 2053 ESTPOAAISRKAVEL 2055 FPVIFSKASEYLQL 2055 FPVIFSKASEYLQL 2056 FPVIFSKASEYLQL 2057 GEALGLYQAQAAFT 2057 GEALGLYQAQAAFT 2058 GLINYAAIMEGD 2069 HLYLLVYRAREPYT 2060 HLYLLVYRAREPYT 2060 HLYLLVYRAREPYT 2061 HLYLLVYRAREPYT 2062 HLYLLVYRAREPYT 2063 HLYLLVYRAREPYT 2064 HLYLLVYRAREPYT 2065 HLYLLVYRAREPYT 2065 HLYLLVYRAREPYT 2066 KTGLJIVAAIMEGD 2066 KTGLJIVAAIMEGD 2066 KTGLJIVAAIMEGD 2067 LGLVGAQAATEGQ 2067 LGLVGAQAATEGQ 2068 LGLVGAQAATEGQ 2070 LLIVAAIMEGDCA 2070 LLIVAAIMEGDCA 2071 LQLVGGIRVVRVPI 2071 LQLVGGIRVARVPI 2071 LQLVGGIRVARVPI 2071 LQLVGGIRVARVPI 2072 LQLVGGIRVARVPI 2073 LQLVGGIRVARVPI 2073 LQLVGGIRVARVPI 2074 MVELVHFLLKYRARE 2077 RAMFPOLESEFQAAI 2077 RAMFPOLESEFQAAI 2077 RAMFPOLESEFQAAI 2077 RAMFPOLESEFQAAI 2077 RAMFPOLESEFQAAI 2077 RAMFPOLESEFQAAI 2078 RALLMQDLVQERYLET 2078 RALLMQDLVQERYLET 2078 RALLMQDLVQERYLET 2078 RALLMQDLVQERYLET 2078 RALLMQDLVQERYLET 2078 RALLMAGATUR 2078 RALLMAGATUR 2078 RALLMQDLVQERYLET 2078 RALLMAGATUR 2078 RALLM | 2023 ESEPÇAAAISKAVPL 1921 0.0067 0.5100 2034 FPVIFSKASEVLQL 1922 2035 FPVIFSKASEVLQL 1922 2035 FPVIFSKASEVLQL 1924 2055 GEALGLVÖQAQANTE 1925 2056 GEALGLVÖQAQANTE 1926 2060 HVTLVTALIMEGDCAP 2060 HVTLVTCLGLSVD 1939 2060 HVTLVTCLGLSVD 1939 2061 HEVVEVVPISHLYIL 1930 2061 HVTLVTCLGLSVD 1931 2062 HVTLVTCLGLSVD 1934 2063 HVTLVTCLGLSVD 1934 2064 KAEMLESVLRNCQDF 1934 2065 KAEMLESVLRNCQDF 1934 2065 KAEMLESVLRNCQDF 1934 2066 KAEMLESVLRNCQDF 1939 2066 KACLUNCALGLSVD 1931 2067 GEVPAADSPPRS 1936 2069 LUTVALIMEGDCA 1939 2070 RVELVHELLKYRARE 1941 2071 LLYKTAREPYTACEM 1941 2071 LLYKTAREPYTACEM 1941 2071 LLYKTAREPYTACEM 1945 2072 RVEVTLGEVPAADSP 1936 2073 LVEVTLGEVPAADSP 1936 2074 RVELVHELLKYRARE 1935 2075 RVEVTLGEVPAADSP 1936 2076 RALESVLRNCQVP 1946 2077 RVEVTLGEVPAADSP 1936 2077 RVEVTLGEVPAADSP 1936 2078 RVEVTLGEVPAADSP 1936 2078 RVEVTLGEVPAADSP 1936 2078 RVEVTLGEVPAADSP 1936 2079 RVEVTLGEVPAADSP 1936 2079 RVEVTLGEVPAADSP 1935 2080 QLYGGEVPEVPVPISH 1931 2081 RVEVTLGEVPAALESVLR 1935 2081 RVEVTLGEVPAALESVLR 1935 2082 REPVTLGEVPAA 1935 2083 RVEVTRIKTLYRARE 1937 2083 RVEVTRIKTLYRARE 1937 2084 RVELIFICATION 1936 2085 VEVTRIKTLYTCCG 1936 2086 VEVTRIKTLYTUTCCG 1936 2089 VEVTRIKTLYTUTCCG 1936 2090 VPGELSVLEYGEE 1934 2093 VTLLTCLGLSYDGLL 1934 2093 VTLLTCLGSYDGLE 1934 2094 VTPLLEER 1935 2095 VTLLTCLGSYDGLE 1934 2096 VTLLTCLGSYDGLE 1934 2097 VTLLTCLGSYDGLE 1934 2096 VTLLTCLGSYDGLE 1934 2097 VTLLTCLGSYDGLE 1934 2096 VTLLTCLGSYDGLE 1934 2097 VT | ER | 2051 | EPHISYPPLHERALR | 1920 | | -0.0011 | | | |
| 2053 EVILGEVRADISPAP 1922 2054 PIVICENTALISPAP 1924 2055 PIVICENTALISPAP 1924 2056 GLAIGUGAPATE 1926 2057 GLIINTALIAREDD 1927 2059 GLIINTALIAREDD 1927 2050 GLIINTALIAREDD 1929 2050 GLIINTALIAREDD 1929 2051 INTALIAREDCAP 1931 2052 GLIINTALIAREDCAP 1931 2054 INTALIAREDCAP 1931 2056 INTALIAREDCAP 1931 2056 KTGLLIIVALIAREDCAP 1935 2056 LIGEVRADISPERPH 1936 2057 GLGVRAATEEQQ 1939 2058 KTGLLIIVALIAREDCAP 1939 2050 LIGEVRADISPERPH 1931 2051 LOEVILGEVRAADSP 1932 2070 LLIXTALIAREDCAP 1934 2071 LUEVILGEVRANDSP 1932 2071 LUEVILGEVRANDSP 1934 2072 LOLUVGENYEVANT 1934 2073 LVEVILGEVRANDSP 1935 2074 MVELVHILKYRAR 1935 2075 RANFPDLESEQAN 1936 2076 RALLEKSASEVI 1936 2077 RANFPDLESEQAN 1937 2078 RALLEKSASEVI 1936 2078 RALLEKYRAELHT 1951 2089 RELLAKTALEKTAR 1935 2081 RELLAKTALET 1935 2081 RELLAKTALET 1935 2081 RELLAKTALET 1935 2082 RELLAKTALET 1935 2083 RELLAKTALET 1935 2084 RELLAKTALET 1935 2085 STITUEVILGENDA 1936 2086 STITUEVILGENDA 1936 2087 VEGENVENDRILL 1936 2088 VEGNFENDRALET 1936 2089 VEGNFENDRALET 1936 2090 VYPISHLYILVTCLG 1936 2091 VEGENVENDRILL 1936 2091 VE | 2053 FFVILGEVRADISPAP 1922 2055 FFVILGEVRADISPAP 1924 2056 GLAIGL/GA/PATE 1926 2057 GLAINAAIAREDD 1927 2058 GLAICL/GA/PATE 1928 2059 HFLILK/RAREPTK 1928 2060 ILINIAAIAREDD 1937 2061 IEVVEVVISHLYII 1930 2061 ILINIAGIOCAPEKUW 1931 2062 IIIAEGDCAPEKUW 1931 2063 IIAIGGDCAPEKUW 1931 2064 ISHLYILYICLGISYD 1934 2065 IIAIGGDCAPATEGO 1939 2066 IIVAAIIAAIAREDDCA 1938 2066 IIVAAIIAAIAGDCA 1938 2067 LGUVGA/PATEGO 1939 2068 LINIAAIAAIAGDCA 1938 2070 LGUVGA/PATEGO 1939 2071 LGUVGA/PATEGO 1939 2071 LGUVGA/PATEGO 1937 2072 LGUVGA/PATEGO 1937 2073 LVEYTICEPYRADISP 1942 2073 LVEYTICEPYRADISP 1943 2074 LALKYRKARELKYRK 1945 2075 LOUVGEVRANTELKYRK 1945 2076 GLUVGA/PATERQO 1937 2077 LGUVGA/PATERQO 1947 2077 LGUVGA/PATERGO 1947 2077 L | KW | 2052 | ESEFQAAISRKMVEL | 1821 | 0.0067 | 0.5100 | 0.0310 | | |
| 2055 FPVIFSKASEYLQLV 2056 GEALGLVGAQARTE 1925 2057 GEALGLVGAQARTE 1925 2058 GEALGLVGAQARTE 1926 2060 GLJITALAIREGD 2060 HLYLLYCRAREPYTK 1928 2060 GLLITALAIREGD 2061 INTALIGEOCAPEKIW 1931 2062 INTALIGEOCAPEKIW 1931 2063 INTALIGEOCAPEKIW 1931 2064 INTALIGEOCAPEKIW 1931 2065 INTALIGEOCAPEKIW 1931 2066 IGVACACAPETEQQ 1932 2066 IGVACACAPETEQQ 1935 2067 IGCVPAADSPSPHS 1935 2068 INTALIAIREGDC 1939 2069 INTALIGEOCAPEKIW 1931 2070 LLITACAIIAIGE 2060 IGVACACAPATEQQ 1939 2060 IGVACACAPATEQQ 1939 2061 ILIVALIAIAIGE 2062 INTALIAIAIGE 2063 INTALIAIAIGE 2064 INTALIAIAIGE 2066 IGVACACAPATEQQ 1939 2067 ILIVALIAIAIGE 2068 IGVACACAPATEQQ 1939 2071 ILIVALIAIAIGE 2072 IVEVTIGEVPAADSP 1941 2073 IVEVTIGEVPAADSP 1942 2073 IVEVTIGEVPAADSP 1945 2074 RALLESEPQAAI 1946 2075 QLVCGENVEVPRI 1946 2076 RALLESEPQAAI 1946 2077 RALLESEPQAAI 1946 2077 RALLESEPQAAI 1946 2078 REVILAMQDLVQENYL 1949 2079 QDFPVIFSKASEYL 1947 2079 QDFPVIFSKASEYL 1947 2079 QDFPVIFSKASEYL 1946 2070 GASEKAVELWFRANTESYLR 1951 2080 SELEINLACHURCHYRAR 1953 2081 RELINIAIIGG 1956 2081 VECHVPRISHL 1955 2081 VECHVPRISHL 1955 2082 VECHVPRISHL 1955 2083 VECHVPRISHL 1955 2084 VECHVPRISH 1955 2085 VECHVPRISH 1955 2086 VECHVPRISH 1955 2087 VECHVPRISH 1955 2089 VECHVPRISH 1955 2080 | 2055 FPVIFENCARELIAN 1972 2056 GEALGLYGAQAPATE 1975 2057 GEALGLYGAQAPATE 1975 2058 GLINTAIIAIEOD 2061 IEVVEVPRISHTYI 1976 2060 IEVVEVPRISHTYI 1970 2061 IEVVEVPRISHTYI 1970 2062 IIVLAIIAIEODCAP 1971 2063 IIVLAIIAIEODCAP 1971 2064 ISHLYILYCLGLSYP 2065 ISHLYILYCLGLSYP 2065 ISHLYILYCLGLSYP 2066 ISHLYILYCLGLSYP 2066 ISHLYILYCLGLSYP 2067 LGEVPAADSPPHS 1975 2068 LGLYGAQAPATEQQ 1977 2069 LUTAIIAIEODCAP 2070 LLIXYARAEODCAP 2071 LLXYARAEODCAP 2071 LLXYARAEODCAP 2072 LUTAIIAIEODCAP 2073 LYAPILGEPAADSP 2074 LUTAIIAIEODCAP 2075 LOEVPAADSPPHS 1940 2077 LLXYARAEOTCAP 2078 QDLYQEPVITSKASET 2078 QULYGEVPEVPRIS 2078 QULYGEVPEVPRIS 2078 GLILIYLAINEGG 2078 VEVYPRILLIYTGC 2078 QULYGELSYDGLL 2078 VEVYPRILLIYTGC 2078 QULYGELSYDGLL 2078 VEVYPRILLIYTGC 2078 VEVYPRILLIYTGC 2078 VEVYPRILLIYTGC 2079 QDLYGENGENGED 2070 VETTURGENGED 2 | AUS FIX | 202 | EVILGEVPADSPSP SEDVIESVASEVI OI | 761 | | | | | |
| 2055 GEALGLVGAQAPATE 1925 2057 GEALGLVGAQAPATE 1926 2059 HELLKYRAREPATK 1928 2060 HLYLLKYRAREPATK 1929 2061 HEVEVPRISHLYIL 1930 2062 GLLINCAINAGEOD 1927 2063 HELLKYRAREPATK 1931 2064 HELLKYRAREPATK 1931 2065 HAVILATIGAGCAP 1932 2065 HAVILATIGAGCAP 1931 2066 HAVILATIALGEOCAP 1932 2066 HAVILATIALGEOCAP 1934 2066 KTGLJINVARIAE 1936 2066 KTGLJINVARIAE 1936 2067 LLINVARIAEOCA 1939 2070 LLINVARIAEOCA 1939 2071 LLINVARIAEOCA 1939 2072 LLINVARIAEOCA 1939 2073 LAUGAVARATE 1941 2073 LAUGAVARATE 1941 2073 LAUGAVARATE 1941 2073 LAUGAVARATE 1941 2073 QLVFGIEVVEVVPI 1949 2073 QLVFGIEVVEVVPI 1949 2073 QLVFGIEVVEVVPI 1949 2073 RALLETSYKKULHT 1951 2080 QLVGENYEVRARE 1955 2081 RALLETSYKKULHT 1951 2081 RALLETSYKKULHT 1951 2082 RALLETSYKKULHT 1951 2083 SHLYILVTCLISYD 1954 2084 STALLYLLOGENYEV 1955 2086 SHLYILVTCLISYD 1954 2087 VECHWOPRALIESY 1955 2088 VECHWOPRALIESY 1955 2089 VEGHEVREVARE 1955 2089 VEGHEVREVARE 1955 2089 VEGHEVREVARE 1955 2080 VEGHEVREVARER 1955 2090 VEGH | 2055 GEALGLVGAQAÄTE 1925 2056 GEALGLVGAQAÄTE 1926 2057 GEALGLVGAQAÄTE 1926 2058 HFLLLKYRAREPVTK 1928 2050 HLYTVTCLGLSYDG 1929 2061 HTLLKYRAREPVTK 1939 2062 HLYTVTCLGLSYDG 1932 2063 HFLLLKYRAREPKLW 1931 2065 KABALESVLRNCQDF 1934 2065 KABALESVLRNCQDF 1934 2065 KABALESVLRNCQDF 1935 2066 KAGALINTARIAEGDCA 1936 2067 LGVVAQAPATEEQQ 1937 2068 LGVGAQAPATEEQQ 1937 2068 LGVGAQAPATEEQQ 1937 2069 LIVALIATIARGDCA 1939 2071 LLKYRAREPVTKAEM 1940 2072 LQVCAGEVVRANDP 1941 2073 LAVTCGEVAASPP 1941 2073 MVELVHFLLKYRAR 1945 2074 MVELVHFLLKYRAR 1945 2075 QAVARKYGLLINTA 1945 2077 PRAFFDLESFQAAI 1946 2077 PRAFFDLESFQAAI 1946 2078 QAVCGEVVEVPYPIS 1950 2077 PRAFFDLESFQAAI 1946 2078 QAVCGEVVEVPNIS 1950 2078 QAVCGEVVEVPNIS 1950 2078 REPVTKAEMLESVLR 1951 2089 VEVYFILLATUALGEVPAA 1955 2089 VEVYFILLATUALGESVBA 1955 2089 VEVYFILLATUALGESVBA 1955 2089 VEVYFILLATUALGESVBA 1950 2080 VETFELVERRALESVLR 1951 2080 VETFERVERED 1950 2081 VETFERVERED 1 | <u> </u> | 205 | FPVIESKASEVI OLV | 1924 | | | | | |
| 2057 GIEVVEVVPISHLYI 2058 GLUTLALIAREDD 2059 H.YILVTCLGLSYDG 2060 H.YILVTCLGLSYDG 2061 IEVVEVVPISHLYI 2062 IIVLAIIAREDCAP 2063 IIVLAIIAREDCAP 2064 IIVLAIIAREDCAP 2065 IIVLAIIAREDCAP 2066 KTGLLIIVLAIIARE 2066 KTGLLIIVLAIIARE 2066 KTGLLIIVLAIIARE 2067 LITVAAIIAREDCA 2070 LLIVAAIIAREDCA 2071 LLKYRAREPYTKAEM 2071 LLKYRAREPYTKAEM 2072 LLIVAAIIAREDCA 2073 LVEVPAADSPSPHS 2074 LLKYRAREPYTKAEM 2075 LLIVAAIIAREDCA 2076 LITVAAIIAREDCA 2077 RVELLMODLVQENYL 2077 LAVELLIIVLAIIARE 2077 LLIVAAIIAREDCA 2077 RVELLMODLVQENYL 2077 PRALLLMODLVQENYL 2077 QAAISRAWAVPISH 2077 RVELLMODLVQENYL 2077 PRALLLMODLVQENYL 2077 RAMEPDLESEFQAAI 2077 PRALLLMODLVQENYL 2077 QAAISRAWAVPISH 2077 RAMEPDLESEFQAAI | 2057 GIEVVEVVPISHLYI 2058 GLUTLAINAREDD 2059 H.YILYCLGLSYDG 2061 IEVVEVVPISHLYI 2062 H.YILYCLGLSYDG 2063 IIYLAIIAREGDCAP 2064 IEVTECACLSYDG 2065 IIYLAIIAREGDCAP 2065 IIYLAIIAREGDCAP 2066 KTGLLIIVAIARE 2066 KTGLLIIVAIARE 2066 KTGLLIIVAIARE 2067 LGEVPAADSISPHS 2068 KTGLLIIVAIARE 2069 LIIVAIIAREGDCA 2070 LLIVAIIAREGDCA 2071 LLIVAIIAREGDCA 2071 LLIVAIIAREGDCA 2072 WVELVPICLIIVA 2073 LVEYTLGEVPAADSP 2074 WVELVPICLIIVA 2075 PRILLMQDLVQENYL 2076 PRILLMQDLVQENYL 2077 RAILEYVPISE 2077 RAILEYVPISE 2077 RAILEYVPISE 2077 RAILEYVPISE 2077 RAILEYVPISE 2078 QULYGERVPVPIS 2079 QDFPVIFSKASEYL 2079 QDFPVIFSKASEYL 2079 QDFPVIFSKASEYL 2079 QDFPVIFSKASEYL 2070 RAILETSYVKULHIT 2070 GLUTLAIARE 2071 RAILTYCLGLSYD 2071 RAILTYCLGLSYD 2071 RAILTYCLGLSYD 2071 RAILTYCLGLSYD 2071 RAILTYCLGLSYD 2071 RAILTYCLGLSYD 2072 RELITSYVKULHIT 2073 REPYTKABALESYLR 2074 RAILTYCLGLSYD 2075 RELITSYVKULHIT 2076 WELNFLLLKYRARE 2077 RAILTYCLGLSYD 2077 RAILTYCLGLSYD 2077 RAILTYCLGLSYD 2077 RAILTYTCLGLSYD 2077 RAILTYCLGLSYD 2077 RAILTY | OAP | 2056 | GEALGI VGAOAPATE | 1925 | | | | | |
| 2058 GLLINVAINAEOD 1927 2069 HFLLKYRAREPVTK 1928 2060 H-YILVTCLGLSY 2061 EVVEVVPISHLYIL 2062 HANTLYTCLGLSY 2063 HYLLKYRAREPVTK 2064 HALLEVLRYAREPWTK 2065 HALLEVLRYAREPWTK 2065 HALLEVLRYAREPWTK 2065 HALLEVLRYAREPWTK 2066 HATTLYTCLGLSY 2066 HATTLYTCLGLSY 2067 HALLEVLRYAREPWTK 2066 HATTLYTCLGLSY 2067 HATTLYTCLGLSY 2068 HATTLYTCLGLSY 2069 HATTLYTCLGLSY 2066 HATTLYTCLGSY 2066 HATTLYTCLGLSY 2066 HATTLYTCLGSY 2067 HATTLYTCLGSY 2067 HATTLYTCLGLSY 2068 HATTLYTCLGLSY 2068 HATTLYTCLGLSY 2069 HATTLYTCLGLSY 2060 HA | 2058 GLLINAAIIAEGD 2061 EVVEVVPISHLYI 2060 IEVVEVVPISHLYI 2061 IEVVEVVPISHLYI 2062 IIALGOCAPEEKW 2064 ISHLYILVTCLGLSY 2065 IIALGOCAPEKW 2064 ISHLYILVTCLGLSY 2065 KAGLIIVAAIIAE 2067 LGEVPAADSPSPHS 2067 LGEVPAADSPSPHS 2068 LGLVGAQAPTEQQ 2070 LLIVAAIIAEGDC 2071 LLIVAAIIAEGDC 2071 LLIVAAIIAEGDC 2071 LLIVAAIIAEGDC 2072 LVEVTLGEVPAADSP 2073 LVEVTLGEVPAADSP 2074 MYELVFEVFFR 2075 PKILLMQDLVQENYL 2076 QDLVGENYVEVPI 2077 RAMPEDLESEPQAI 2077 PKAREVTRAE 2078 QDLVGENYLEVFR 2078 QDLVGENYLEVFR 2079 QDLVGENYLEVFR 2070 QLVGENYLEVFR 2071 LLIVAAIIAEGDC 2071 LLIVAAIIAEGDC 2072 LVEVTLGEVPAADSP 2073 LVEVTLGEVPAADSP 2074 MYELVFELKYRAR 2075 QDLVGENYLEVFR 2076 RALLETSYVKLHFT 2077 RAMPEDLESEPQAI 2077 PKAREVTLGEVPA 2077 CQLGENYLEVFR 2077 CQLGENYLE 2077 CQLGENYLEVFR 2 | ISH. | 2057 | GIEVVEVVPISHLYI | 1926 | 0.0710 | 0.0900 | 6800.0 | | |
| 2059 HFLLLKYRAREPVTK 1928 2060 HLYTCLGLSYDG 1929 2061 IEVVEVPRISHT 1931 2062 IIAEGDCAPEEKIW 1931 2063 IIALAILATGGGAP 1932 2064 IHALYILYCIGLSY 1933 2065 KAEMLESVLRNCQDF 1934 2066 KAEMLITATAILIE 1935 2067 LGEVPAADSPSPHS 1936 2068 LGLVGAQAPATEEQQ 1937 2070 LGLYRARAEPYTKAEM 1940 2071 LLKYRAREPYTKAEM 1940 2071 LLKYRAREPYTKAEM 1941 2072 LOLYGIEVVEVYPI 1942 2073 LLKYRAREPYTKAEM 1946 2073 LLKYRAREPUTKAEM 1945 2073 LUKYRYRTGLLINYA 1945 2073 LANPPRINTESKASEYL 1948 2073 QAAISRKWYELVHT 1951 2073 QALVEGIEVVEVYPIS 1945 2073 QALSKASEYL 1948 2073 <td< td=""><td>2059 HFLLKYRAREPVTK 1928 2060 HINTYCLGLSYDG 1929 2061 IEVVEVPRISHT 1931 2062 IIAEGDCAPEEKIW 1931 2063 IIALAILAGGGCAP 1932 2064 SHLYILYGLGLSY 1933 2065 KAEMLESVLRNCQDF 1934 2066 KAEMLESVLRNCQDF 1934 2067 LGEVPAAPSEPHS 1936 2068 LGLVGAQARATEGQ 1935 2068 LGLVGAQARATEGQ 1936 2070 LLITVAIALEGDCA 1938 2071 LLKYRAREPYTKAEM 1940 2071 LLKYRAREPYTKAEM 1941 2072 LQLVGIEVVEVVPI 1942 2073 LQLVFGIEVVEVVPI 1943 2074 PRMIPDLESECAL 1946 2075 PRMIPDLESECAL 1946 2075 PRAMIPDLESECAL 1945 2078 QALDERVKEVPRIS 1945 2079 QUEVEGEVTEVPRIS 1945 2081 RELINGE</td><td>_</td><td>2058</td><td>GLLITVLAIIAIEGD</td><td>1927</td><td></td><td>-0.0011</td><td></td><td></td><td></td></td<> | 2059 HFLLKYRAREPVTK 1928 2060 HINTYCLGLSYDG 1929 2061 IEVVEVPRISHT 1931 2062 IIAEGDCAPEEKIW 1931 2063 IIALAILAGGGCAP 1932 2064 SHLYILYGLGLSY 1933 2065 KAEMLESVLRNCQDF 1934 2066 KAEMLESVLRNCQDF 1934 2067 LGEVPAAPSEPHS 1936 2068 LGLVGAQARATEGQ 1935 2068 LGLVGAQARATEGQ 1936 2070 LLITVAIALEGDCA 1938 2071 LLKYRAREPYTKAEM 1940 2071 LLKYRAREPYTKAEM 1941 2072 LQLVGIEVVEVVPI 1942 2073 LQLVFGIEVVEVVPI 1943 2074 PRMIPDLESECAL 1946 2075 PRMIPDLESECAL 1946 2075 PRAMIPDLESECAL 1945 2078 QALDERVKEVPRIS 1945 2079 QUEVEGEVTEVPRIS 1945 2081 RELINGE | _ | 2058 | GLLITVLAIIAIEGD | 1927 | | -0.0011 | | | |
| 2060 HLYILVTCLGLSYDG 2061 IGNEDCAPERKYIL 2063 IGNEDCAPERKYIL 2064 IGNEDCAPERKYIL 2065 IGNEDCAPERKYIL 2066 IGNEDCAPERKYIL 2066 IGNEDCAPERKYI 2066 IGNEDCAPERKYI 2066 KAEMLEYLRYODF 2066 KTGLIUTALINE 2066 KTGLIUTALINE 2067 IGLVAQAPTEQQ 2068 LGLVAQAPTEQQ 2068 LGLVAQAPTEQQ 2068 LGLVAQAPTEQQ 2069 LITVLAINAEGDC 2070 LLKYRAEPYTKAEM 1940 2071 LLKYRAEPYTKAEM 1941 2071 LLKYRAEPYTKAEM 1942 2072 LVEVTLGEVPADSP 2073 LVEVTLGEVPADSP 2074 WYELLKYRAR 2076 PRMFDLESFQAAI 2077 PRMFDLESFQAAI 2077 QDFPVIFSKASTV 2077 QDFVIFSKASTV 2078 QAAISKRWELVHFL 2079 QDFVVENYIS 2070 QDLVGEVVEVYPIS 2071 QLVGEVVEVYPIS 2071 GLLIVLAINAEG 2072 RALLIKYRAR 2073 RALLIKYRAR 2074 QDLVGEVVEVYPIS 2075 GLVGEVVEVYPIS 2076 GLVGEVVEVYPIS 2077 GLLIVLAINAEG 2077 GLLIVLAINAEG 2078 RELLIKYRARE 2078 SHLYILVTCLGLSYD 2078 VEVEYRHYILLKYRARE 2078 VEVEYRHYILLKYRARE 2079 VFGIEVVEVYPISH 2070 VFGIEVVEVYPISH 2071 VYPISHLYILLKYRARE 2071 VYPISHLYILLTGYTS 2072 VFELLIVAGIESTY 2073 VFELLIVAGIESTY 2074 VILVTCLGLSYDGLL 2075 VFELLIVAGIESTY 2076 VFELLIVAGIESTY 2077 VILVTCLGLSYDGLL 2077 VFELLIVAGIESTY 2077 VFELLIVAGIESTY 2077 VILVTCLGLSYDGLL 2077 VILVTCLGLSYDGL | 2060 H.VILYOLGLSYDG 1929 2061 IEVVEVPRIRLYIL 1930 2063 IIAVLAIIAREGDCAP 1932 2064 SHLTYLYCLGLSY 1933 2065 SHLTYLYCLGLSY 1933 2066 KAEMLESVATKOOPF 1933 2066 KTGLLIIVALAIIAIE 1935 2067 LGLVGAQAPATENERPRO 1937 2068 LGLVGAQAPATENERPO 1933 2069 LIIVAAIIAIEGDCA 1933 2070 LGLVGAQAPATENEQQ 1933 2071 LLKYRAREPYTKAEM 1940 2071 LLKYRAREPYTKAEM 1941 2071 LLKYRAREPYTKAEM 1942 2071 LUKYRAREPYTKAEM 1943 2072 LQLVFGIEVVEVPR 1945 2073 NQVMRYTGILIIVAA 1945 2074 AVELINQOLVGENTERRA 1945 2075 QDFFPVIFSKASEYL 1946 2078 QDFFPVIFSKASEYL 1945 2078 QLVFGIEVVEVPRINT 1945 20 | REP | 2059 | HFLLLKYRAREPVTK | 1928 | | | | | |
| 2061 IEVVEVVPISHLYII. 1930 2063 IIALYAIAREDKAPEKW 1931 2064 IIALYAIAREDKAPEKW 1932 2064 ISHLYILYTCLGLSY 1933 2065 KAEMLESYLRNCQDF 1934 2066 KTGLLIIVLAIIARE 1935 2067 LGEVRAADSPSPRIS 1937 2068 LITVAIIAREDCA 1938 0.0130 2070 LLITVAIIAREDCA 1939 0.0130 2071 LLKYRAREPYTKAEM 1940 0.0130 2072 LLIVEATIGECRAADSP 1941 -0.0011 2073 LLYEVILGEVRANDSP 1943 -0.0011 2073 LLYEVILGEVRANDSP 1943 -0.0011 2073 LOVYREKTGLLIIVLA 1945 -0.0011 2074 MYNARKTGLLIIVLA 1945 -0.0011 2075 PRALLMODLVQENYL 1945 -0.0011 2076 QDFFPVIFSKASEYL 1946 -0.0011 2077 QDFFPVIFSKASEYL 1946 -0.0011 2078 | 2061 IEVVEVVPISHLYIL 1930 2063 IIALEOLOAPEEKIW 1931 2064 IIALEOLOAPEEKIW 1931 2065 IIALEOLOAPEEKIW 1933 2066 KTGLLIVLAINEDCOAP 1935 2066 KTGLLIVLAINEDCOAPEKINSODF 1935 2066 KTGLLIVLAINEDCOA 1937 2067 LGEVPAADSPSPHS 1936 2070 LLIVTAAIIAEGDCA 1939 2070 LLIVTAAIIAEGDCA 1939 2070 LLIVTAAIIAEGDCA 1939 2071 LLIVTAAIIAEGDCA 1940 2071 LLIVTAAIIAEGDCA 1940 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPAVPI 1941 2073 LVEVTLGEVPAVPI 1945 2074 MVELVHFLLLKYRAR 1944 2077 PRAKLLMQDLVQENYL 1948 2077 PRAKLLMQDLVQENYL 1948 2077 PRAKLLMQDLVQENYL 1948 2078 QLVFGIEVVEVVPIS 1950 2078 QLVFGIEVVEVVPIS 1951 2081 QLVFGIEVVEVVPIS 1951 2082 RALIETSYKVLHFT 1951 2083 REPYTKAEMESPL 1955 2084 RKLLMQDLVQENYLE 1955 2085 STILYTLGESPP 1955 2086 VELVHFLLKYRARE 1955 2087 TGLLIVLAIAREE 1955 2088 VELVHFLLKYRARE 1955 2089 VFGIEVVEVPRARE 1955 2089 VFGIEVVEVPRARE 1955 2089 VFGIEVVEVPRARE 1956 2091 VPRISHLYILYTCLG 1956 2091 VFGIEVVEVPRARE 1957 2092 VFGIEVVEVPRARE 1957 2093 YFFLHERALREGEE 1967 2093 YFFLHERALREGEE 1964 2095 YFFLHERALREGEE 1964 2095 YFFLHERALREGEE 1964 | STS | 2060 | HLYILVTCLGLSYDG | 1929 | | | | | |
| 2062 IIAJEGDCAPEKIW 1931 2063 IIAJAIRGEDCAP 1932 2064 KAEMLESVLRNÇQDF 1934 2065 KAEMLESVLRNÇQDF 1934 2066 KAGILINYALIIARE 1935 2067 LGEVPAADSPSPPHS 1936 2068 LIIVLAIIAREGAC 1938 2070 LLIIVLAIIAREGAC 1940 2071 LLKYRAREPYTKAEM 1940 2071 LLKYRAREPYTKAEM 1940 2072 LQLVFGIEVVEVVPI 1941 2073 LVEYTLGEVPAADSP 1943 2074 MNELLIKYRAER 1944 2075 LQLVFGIEVVEVVPI 1945 2074 MNELLIKYRAER 1946 2075 RALLICKYRAERYRAERY 1946 2076 PRKLLMQDLVQENYL 1946 2077 PRKKRAVELVHT 1946 2078 QDEFPVIFSKASEY 1946 2079 QDEFVIFSKASEY 1946 2070 QDEFVIFSKASEY 1947 2081 | 2062 IALEGDCAPERKW 1931 2062 IALEGDCAPERKW 1932 2063 IVAININGOLAP 1932 2064 INVAININGOLAP 1932 2065 INVAININGOLAP 1934 2065 INVAININGOLAP 1934 2066 LIGEVARADSPSPRIS 1936 20011 2067 LGEVARADSPSPRIS 1936 2017 LINYARAREPYTREQQ 1937 2017 2017 LINYARAREPYTREQQ 1937 2017 LINYARAREPYTRAEM 1941 2073 LUKYTRAREPYTRAEM 1942 2073 LUKYTRAREPYTRAEM 1942 2073 LUKYTRAREPYTRAEM 1944 -0.00111 2073 LUKYTRAREPYTRAEM 1945 2073 LUKYTRAREPYTRAEM 1945 2074 AVELUMQDLVQENYL 1945 2075 QDEPSPVIRSKAST 1946 2076 QDEVQENYLEYRQVP 1947 2076 QDEPSPVIRSKAST 1947 2076 QDEVQENYLEYRQVP 1947 2076 QDEVQENYLEYRQVP 1950 2080 QULVQENYLEYRQVP 1951 2080 QULVGENYEYRRE 1952 2081 TGLLINYALIAEG 1956 2080 VEVPISHLYTIC 1956 2080 VEVPISHLYTIC 2090 VETLUMQDLVQENYLE 2060 VETLUMGRALEFORED 1961 2091 VETLUMGRALEFORED 2095 VETLUMGRALEFORED | VEVVPISHL | 2061 | IEVVEVVPISHLYIL | 1930 | | | | | |
| 2063 IIVLAIIAIEGDCAP 1932 2064 ISHLYILYCIGLSY 1933 2065 KAEMLESYURIQQIF 1934 2066 KTGLIIVLAIIAIE 1935 0.0015 2067 LGEVPAADSPSPHS 1936 -0.0011 2069 LIIVLAIIAIEGDC 1939 0.0130 2071 LLIKYRAREPYTKAEM 1940 0.0130 2071 LLIKYRAREPYTKAEM 1943 -0.0011 2071 LLIKYRAREPYTKAEM 1943 -0.0011 2071 LLIKYRAREPYTKAEM 1943 -0.0011 2072 LQLYGEIVVEVVPI 1943 -0.0011 2073 LUVFGILVEVVPI 1945 -0.0011 2074 MVELLMQDLVGENYL 1946 -0.0011 2075 PRIKLINGULVEVVPI 1945 -0.0011 2076 QAAISRKMVELVHIT 1945 -0.0011 2077 QULVGENYLEYRQVP 1949 -0.0011 2080 QULVGENYLEYRQVP 1950 -0.0011 2081 RKLLMQDLGSPALEYRQVP | 2063 IIVLAIIAIEGDCAP 1932 2064 ISHLYILVTCLGLSY 1933 2066 KTGLLIVTCLGLSY 1933 2066 KTGLLIVTCLGLSY 1934 2067 LGEVRAADSPSPPHS 1936 2068 LGLVGARATEGQC 1937 2068 LGLVGARATEGQC 1937 2069 LITVLAIIAIGGCC 1939 2070 LLITVLAIIAIGGCC 1939 2071 LLITVLAIIAIGCCC 1939 2071 LLITVLAIIAIGCCC 1940 2071 LLITVLAIIAIGCCC 1941 2072 LUTVTGEVVAVPI 1943 2073 LVEVTLGEVPAADSP 1943 2074 PRAMFDLESEFQAAI 1946 2075 PRAMFDLESEFQAAI 1948 2077 PRAMFDLESEFQAII 1948 2078 | PEE | 2062 | IIAIEGDCAPEEKIW | 1931 | | | | | |
| 2064 ISHLYILYTCLGLSY 1933 2065 KABMLESVLRNCQDF 1934 0.00290 2066 KAGLINYARIAHE 1935 0.0011 2067 LGEVGAQARATEQQ 1936 -0.0011 2068 LINYARIAHEGDC 1939 0.0130 2070 LLINYARIAHEGDC 1939 0.0130 2071 LLKYRAREPYTKAEM 1940 -0.0011 2072 LUKYTLGEVPAADSP 1942 -0.0011 2073 LVEYTLGEVPAADSP 1943 -0.0011 2074 MYELLIKYRAR 1944 -0.0011 2075 ROVAMPKTGLLINYA 1945 -0.0011 2075 ROVAMPKTGLLINYA 1946 -0.0011 2076 AGASRAWAEVHT 1946 -0.0011 2077 PRMFPDLESEFQAAI 1946 -0.0011 2078 QAASIRKAWALHHT 1951 208 2080 QUVGEVVEVVRIAHT 1951 208 2081 QLVFGIEVVEVVRIAHT 1954 -0.0011 2082 | 2064 ISHLYILVTCLGLSY 1933 2065 KABMLESVLRNCQDF 1934 0.0015 2066 KAGLINVARIARIE 1935 0.0011 2066 LGLVGAQAPATEEQQ 1937 0.0011 2068 LGLVGAQAPATEEQQ 1937 0.0120 2069 LINYARIAEGDCA 1939 0.0130 2071 LLKYRAREPYTKAEM 1940 0.0130 2072 LQLVFGIEVVEVVPI 1941 -0.0011 2073 LVFCTIGEVPANDSP 1942 -0.0011 2074 AWELVHFLLLKYRAR 1944 -0.0011 2075 LQLVFGIEVVEVVPI 1945 -0.0011 2076 PRKLLMQDLVQENYL 1946 -0.0011 2077 PRKLLMQDLVQENYL 1946 -0.0011 2078 QDFPVIFSKASEY 1946 -0.0011 2079 QDFPVIFSKASEY 1946 -0.0011 2070 QUFOIEVVEVVEV 1951 -0.0011 2081 RALLIKYRVEVEVPIR 1955 -0.0011 2082< | 6 | 2063 | IIVI AIIAIEGDCAP | 1932 | | | | | |
| 2065 KAEMLESVLRNCQDF 1934 0.0015 0.0290 2066 KTGLUIVLAIIAIE 1935 0.0015 0.0010 2067 LGLVGAQAPATEEQQ 1936 -0.0011 2069 LIIVLAIIAIEGDCA 1938 0.0120 2070 LLIIVLAIIAIEGDCA 1939 0.0130 2071 LLIKYRAREPYTKAEM 1940 -0.0011 2072 LQLYFGIEVVEVPR 1941 -0.0011 2073 LVEVTLGEVPAADSP 1942 -0.0011 2074 MVELVHFLLKYRAR 1943 -0.0011 2074 MVELVHFLLKYRAR 1945 -0.0011 2075 MVELVHFLLLKYRAR 1945 -0.0011 2076 PRKLLMQDLVQENYL 1945 -0.0011 2077 PRMFPDLESEFQAB 1945 -0.0011 2078 QDFFPVIFSKASEYL 1948 -0.0011 2079 QDFFPVIFSKASEYL 1949 -0.0011 2081 RALLETSYVKVLHHT 1952 -0.001 2084 RKLLMQDVENYLE | 2665 KAEMLESVIRNCQDF 1934 2666 KTGLLINVAIIAIE 1935 0.0015 0.0230 2667 LGEVPAADSRSPHS 1936 0.0015 0.0011 2068 LGEVPAADSRSPHS 1936 0.0013 2068 LGLVGAQAPATERQQ 1937 0.0120 2070 LLINVAIIAIEGDCA 1939 0.0130 2071 LLIVRAREPYTKAEM 1940 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPAADSP 1943 2074 MVELVHFLLLKYRAR 1945 2075 MVELVHFLLKYRAR 1945 2076 PRILLMQDLVGENYL 1945 2077 QDLVGEVVEVVPI 1949 2077 QDLVGEVVEVVPI 1949 2078 QAAISRXMVELWIL 1951 2078 QAAISRXMVELWIL 1951 2080 QDLVGENYLEVRQVP 1953 2081 RELITIVACICLSVIR 1955 2081 RELITIVACICLSVIR 1955 2082 RALLETSVYKVLHHT 1951 2083 RELITIVACICLSVIR 1955 2084 RKLLMQDLVGENYLE 1955 2085 STLVEVTLGEVPAA 1956 2086 STLVEVTLGEVPAA 1956 2087 VEVYPISHLYILVTCC 1958 2088 VEVYPISHLEVERGEE 1956 2090 VYGIEVVEVPISHL 1959 2091 VYPISHLYILVTCLG 1959 2092 VRELSMCRALEFFERED 1961 2093 YTELWGRALIEFTS 1961 2093 YTELWGRALIEFTS 1964 | 2 | 2064 | ISHI VII VTCI GI SV | 1933 | | | | | |
| 2066 KTGLLINLARIME 1935 0.0015 0.0290 2067 LGEVPAADSPSPHS 1936 0.0015 2068 LGLVGAQARTEEQQ 1937 0.0120 2070 LLIVLAILAIEGDCA 1939 0.0130 2071 LLKYRAREPVTKAEM 1940 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPAADSP 1942 2073 LVEVTLGEVPAADSP 1942 2074 MVELVHFLLIKYRAR 1943 2075 MVELVHFLLIKYRAR 1944 2076 PRIKLLMQDLVQENYL 1945 2077 PRAFPDLESEPQAAI 1946 2077 PRAFPDLESEPQAAI 1946 2077 PRAFPDLESEPQAAI 1946 2078 QALSKKMVELVHFL 1947 2079 QALSKKMVELVHFL 1947 2070 QDLVQENYLETRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2081 QLVFGIEVVEVPIS 1951 2082 RALLINQDLVQENYLE 1955 2083 SHLYILVTCIGLSVD 1954 2084 RKLLMQDLVQENYLE 1955 2085 SHLYILVTCIGLSVD 1954 2086 SSTLVEYTLGEVPAA 1955 2087 VEVVPISHLYILLKYRARE 1957 2089 VEVVPISHLYILLKYRARE 1956 2090 VFGIEVVEVVPISHL 1960 2091 VVPISHLYILVTCLG 1958 2094 YILVTCLGLSVDCLL 1965 2094 YILVTCLGLSVDCLL 1965 2094 YILVTCLGLSVDCLL 1965 | 2066 KTGLLINLALIAIE 1935 0.0015 2067 LGEVPAADSPSPHS 1936 -0.0011 2068 LGLVGAQAPATEQQ 1937 -0.0011 2069 LITVLAILAIGGDCA 1939 0.0130 2071 LLIKYRAREPVTKAEM 1940 0.0130 2071 LLIKYRAREPVTKAEM 1941 -0.0011 2072 LQLVGIEVVEVVPI 1942 -0.0011 2073 LVEVTLGEVPAADSP 1942 -0.0011 2074 MVELVHFLLKYRAR 1943 -0.0011 2075 MQVMPKTGLLINUA 1946 -0.0011 2076 PRKLLMQDLVQENYL 1946 -0.0011 2077 PRMFPDLESEFQAAI 1946 -0.0011 2078 QAAISRKAVELVHT 1946 -0.0011 2079 QDFFPVIFSKASEYL 1946 -0.0011 2080 QDLOGENYLEYPIS 1950 -0.0011 2081 RELTINGLOKENYLEYPIS 1953 -0.0011 2082 STLVEVTRALEGRED 1954 -0.0011 | CNG | 2065 | K A EMI ESVI BNCODE | 1934 | | | | | |
| 2067 LGEVPAADSPSPPHS 1936 -0.0011 2068 LGLVGAQAPATEEQQ 1937 -0.0011 2069 LINVAIIAIEGDCA 1939 0.0120 2070 LLIKYRAREPVTKAEM 1940 0.0130 2071 LLKYRAREPVTKAEM 1940 -0.0011 2073 LVEVTLGEVPEVPH 1941 -0.0011 2074 MVELVHFLLKYRAR 1943 -0.0011 2075 NQVMPKTGLLIIVLA 1944 -0.0011 2076 NQVMPKTGLLIIVLA 1945 -0.0011 2077 NQVMPKTGLLIIVLA 1945 -0.0011 2078 QAAISRKMVELVHT 1946 -0.0011 2078 QDFFPVIFERKASEYL 1949 -0.0011 2080 QULVGGEVVEVPRIS 1950 -0.0011 2081 RALLIETSYWKJLHT 1951 -0.0011 2082 RALLIETSYWKJLHT 1953 -0.0011 2083 REPVTKAEMLESVLR 1954 -0.0011 2084 WELLIMQDLVQENPA 1954 -0.0011 | 2067 LGEVPAADSPSPHS 1936 -0.0011 2068 LGLVGAQPATEEQQ 1937 -0.0011 2069 LITIVLAIIAIEGDCA 1938 0.0130 2070 LLIKYRAREPUTKARIM 1940 0.0130 2071 LQLVFGIEVVEVVPI 1941 -0.0011 2072 LQLVFGIEVVEVVPI 1943 -0.0011 2073 LVEVTLGEVPAADSP 1944 -0.0011 2074 MVELVHFLLIKYRAR 1944 -0.0011 2075 PRKLLMQDLVQENYL 1945 -0.0011 2076 PRAJERKANYELYHT 1946 -0.0011 2077 PRAJERSKANSEYL 1948 -0.0011 2078 QDLVGENYLEYRQVP 1949 -0.0011 2080 QDLVGENYLEYRQVP 1948 -0.0011 2081 QLVFGIEVVEVVPIS 1951 -0.0011 2081 QLVFGIEVVEVVPIS 1952 -0.0011 2082 STLLWFLILKORL 1954 -0.0011 2084 VELLINTALLEGE 1954 -0.0011 |) | 9902 | KTGI I IIVI AIIAIE | \$261 | 0.0015 | 0 0200 | -0 0004 | | |
| 2069 LGLVGARATEEQQ 1937 2069 LITVLAIIAIEGDCA 1938 2070 LLIVYLAIIAIEGDCA 1939 2071 LLKYRAREVTKAEM 1941 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPABDSP 1942 2073 LVEVTLGEVPABDSP 1943 2075 MVELVHFLLKYRAR 1944 2075 MVELVHFLLKYRAR 1945 2076 PRKLLMQDLVQENYL 1945 2077 PRKLLMQDLVQENYL 1945 2077 PRKLLMQDLVQENYL 1946 2077 PRKLLMQDLVQENYL 1948 2077 QDFFVIFSKASEYL 1947 2079 QDFFVIFSKASEYL 1948 2070 QDLVFGIEVVEVVPIS 1951 2081 QLVFGIEVVEVVPIS 1951 2082 RALIETSYVKVLHHT 1951 2082 RALIETSYVKVLHHT 1951 2084 RKLLMQDLVQENYLE 1953 2084 STLVTLXTCLGLSYD 1954 2087 TGLLIIVLAIIAIEG 1956 2087 VELVHFLLLKYRARE 1955 2087 VELVHFLLKYRARE 1955 2090 VFGIEVVEVPISHL 1959 2091 VVPISHLYILVTC 1950 2091 VVPISHLYILVTCLG 2093 YEFLWGPRALIETSY 1963 2094 VYILVTCLGLSYDGLL 1963 | 2069 LGLVGARATERQQ 1937 2069 LINVLAIIAIEGDCA 1938 2070 LLINVLAIIAIEGDCA 1939 2071 LLKYRAREVTKAEM 1941 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEVPABDSP 1942 2073 LVEVTLGEVPABDSP 1943 2075 MVELVHFLLKYRAR 1944 2075 MVMPKTGLLIIVLA 1945 2076 PRMFPDILESEFQAAI 1945 2077 PRMFPDILESEFQAAI 1946 2077 PRMFPDILESEFQAAI 1946 2077 PRMFPDILESEFQAAI 1947 2078 QDFFVIFSKASEYL 1948 2079 QDFFVIFSKASEYL 1948 2070 QDFFVIFSKASEYL 1951 2081 QLVFGIEVVEVVPIS 1951 2082 RALIETSYVKVLHHT 1951 2082 RALIETSYVKVLHHT 1951 2082 RALIETSYVKVLHT 1951 2083 STLVILVTCLGLSYD 1954 2084 VELVHFLLLKYRARE 1955 2086 VELVHFLLKYRARE 1955 2080 VEGIEVVEVPISHL 1977 2090 VFGIEVVEVPISHL 1977 2091 VVPISHLYILVTCLG 1960 2092 VEFLWGPRALIETSY 1965 2093 YEFLWGPRALIETSY 1965 2094 YPPLHERALREGEE- 1964 | Coco | 2067 | 1 GEVPA A DOPOPHO | 1936 | | 0.00 | | | |
| 2009 LINYARATATATATATATATATATATATATATATATATATATA | 2006 LINYARATATATATATATATATATATATATATATATATATATA | 15.6 | 907 | COLVENOVO NO TEEDO | 1027 | | | | | |
| 2070 LINTAHARIAGUAA 2071 LLKYRAREPYTKAEM 1940 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLGEPRAADSP 1942 2073 LVEVTLGEPRAADSP 1943 2074 MVELVHFLLKYRAR 1944 2076 MVELVHFLLKYRAR 1944 2076 PRALFDLESEFQAAI 1946 2077 PRMFPDLESEFQAAI 1946 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKMVELVHFL 1947 2079 QDFFPVIFSKASEYL 1949 2079 QDFFPVIFSKASEYL 1949 2070 QDFFPVIFSKASEYL 1949 2070 QDFFPVIFSKASEYL 1949 2071 QLLVFGIEVVEVVPIS 1950 2081 REPVTKAEMLESVLR 1951 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1955 2084 STILVEVTLGEVPAA 1955 2085 STILVATLGEVPAA 1955 2086 VELVHFLLLKYRARE 1957 2087 VELVHFLLKYRARE 1957 2089 VEVVPISHLYILVTC 1959 2091 VVPISHLYILVTC 1950 2093 VEFLWGPRALIETSY 1963 2094 VYPISHLYILVTCLG 1960 2093 YEFLWGPRALIETSY 1963 | 2070 LINTAHAREUTA 1930 2071 LLKYRAREPYTKAEM 1940 2072 LQLVFGIEVVEVVPI 1941 2073 LVEVTLCEVPAADSP 1942 2074 MYELVKYRAR 1943 2075 MYELLKKYRAR 1944 2076 MYELVHTLAR 1944 2077 PRMFPDLESEFQAAI 1946 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKMVELVHFL 1947 2078 QAAISRKMVELVHFL 1947 2079 QDFFPVIFSKASEYL 1949 2070 QDFFPVIFSKASEYL 1949 2070 QDFFPVIFSKASEYL 1949 2071 PRMFPDLESEFQAAI 1950 2081 REPVTKAEMLESVLR 1951 2082 RALLENSYWKLHHT 1951 2083 REPVTKAEMLESVLR 1955 2083 REPVTKAEMLESVLR 1955 2084 KKLLMQDLVQENYLE 1955 2085 STLVEVTLGEVPAA 1955 2086 VELVHFLLKYRARE 1957 2087 VELVHFLLKYRARE 1957 2089 VEGIEVVEVPISHLYILVTC 1958 2090 VFGIEVVEVPISHLYILVTC 1950 2090 VFGIEVVEVPISHLYILVTC 1960 2091 YEFLWGPRALIETSY 1960 2092 YEFLWGPRALIETSY 1960 2093 YEFLWGPRALIETSY 1960 2094 YILVTCLGLSYDGLL 1964 | 377 | 7000 | TOTACATATETICAL | 1020 | | 00100 | | | |
| 2070 LLINYAREPYTKAEM 1940 2071 LLKYRAREPYTKAEM 1940 2072 LQLVFGIEVVRVPT 1941 2073 LVEVTLGEVPAADSP 1942 2074 MVELVHFLLKYRAR 1943 2075 MVVMPKTGLLINYA 1945 2076 PRKLLMQDLVGENYL 1945 2077 PRMFPDLESEFQAAI 1946 2077 PRMFPDLESEFQAAI 1946 2078 QAAISKKMVELVHFL 1947 2078 QAAISKKMVELVHFL 1947 2080 QDLVGENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2081 QLVFGIEVVEVVPIS 1951 2082 RALLETSYWKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVGENYLE 1953 2084 SSTLVEVTLGEVPAA 1955 2085 SSTLVEVTLGEVPAA 1955 2087 TGLLINYAIAIEG 1956 2090 VFGIEVVPISHLYILVTCLG 1950 2091 VVPISHLYILVTCLG 1960 2091 VVPISHLYILVTCLG 1960 2093 YEFLWGPRALIETSY 1963 2094 YFELWGPRALIETSY 1963 | 2070 LLIIVARAREPVTKAEM 1939 2071 LLKYRAREPVTKAEM 1940 2073 LVEVTLGEVPAADSP 1942 2073 LVEVTLGEVPAADSP 1943 2074 MVELVHFLLKYRAR 1943 2075 MVANPKTGLLIIVIA 1944 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKAVELVHFL 1947 2079 QDFPVIFSKASEYL 1949 2080 QDLVGENYEVVPIS 1950 2081 REPVTKAEMLESVLR 1951 2082 RALLETSYWKU-HHT 1951 2083 REPVTKAEMLESVLR 1955 2084 RKLLMQDLVQENYLE 1955 2084 RKLLMQDLVQENYLE 1955 2085 SHLYILVAIGAEG 2086 VELVHFLLKYRARE 1955 2087 VELVHFLLKYRARE 1955 2089 VELWFLLKYRARE 1955 2090 VFGIEVVEVYPISHL 1960 2090 VFGIEVVEVYPISHL 1960 2091 YFELWGPRALETSY 1960 2092 YFELWGPRALETSY 1963 2093 YFELWGPRALETSY 1963 2094 YILVTCLGLSYDGLL 1964 | 2 : | 6907 | LIIVLAIIAIEGDCA | 1930 | | 0.0120 | | | |
| 2071 LUNTKAREPY INAEM 2072 LQLYFGIEVVEVPP 2073 LVEVTLCEPPAADSP 2073 LVEVTLCEPPAADSP 2075 MVELVHFLLKYRAR 2076 MVVMPKTGLLIIVIA 2076 PRKLLMODLVGENYL 2077 PRMFPDLESEFQAAI 2077 PRMFPDLESEFQAAI 2078 QAAISKKMVELVHFL 2080 QDLVGENYLEYRQVP 2081 QLVFGIEVVEVVPIS 2081 QLVFGIEVVEVVPIS 2082 RALIETSYVKVLHHT 2082 RALIETSYVKVLHHT 2082 RALIETSYVKVLHHT 2083 REPVTKAEMLESVLR 2084 RKLLMQDLVGENYLE 2085 STLVEVTLGEVPAA 2086 SSTLVEVTLGEVPAA 2087 TGLLIIVLAIAIEG 2087 VELVHFLLLKYRARE 2088 VELVHFLLLKYRARE 2089 VELVHFLLLKYRARE 2090 VFGIEVVEVPISHL 2091 VVPISHLYILVTC 2090 VFGIEVVEVPISHL 2093 YEFLWGPRALIETSY 2094 VYILVTCLGLSYDGLL 2095 YEFLWGPRALIETSY 2095 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YILVTCLGLSYDGLD 2097 YILVTCLGLSYDGLD 2097 YILVTCLGLSYDGLD 2097 YILVTCLGLS | 2071 LUNTKAREPY INAEM 2072 LQUYFGIEVVEVVPI 1941 2073 LVEVTLCEVPAADSP 1942 2073 MVELVHFLLKYRAR 1943 2075 MVVMPKTGLLIIVLA 1944 2076 PRKLLMQDLVGENYL 1945 2077 PRMFPDLESEFQAAI 1946 2077 PRMFPDLESEFQAAI 1946 2077 PRMFPDLESEFQAAI 1946 2078 QAAISKKMVELVHFL 1947 2079 QDFFPVTEKARASEYL 1949 2081 QUVFGIEVVEVVPIS 1950 2081 QUVFGIEVVEVVPIS 1951 2082 RALIETSYVKVLHHT 1951 2083 REPYTKAENLESVLR 1953 2084 RKLLMQDLVGENYLE 1953 2085 STLYTUVTCLGLSVD 1954 2086 STLYTUVTCLGLSVD 1956 2087 TGLLIIVLAIIAIEG 1956 2087 VELVHFLLLKYRARE 1957 2098 VEVVPISHLYILVTC 1959 2091 VVPFISHLYILVTCLG 1960 2092 VEFLWGPRALIETSY 1965 2093 YEFLWGPRALIETSY 1964 2094 YTILVTCLGLSYDGLL 1964 | i i | 2070 | LLIIVEAIIAIBODO | 6661 | | 0.0100 | | | |
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| 2074 MVELVHFLLKYRAR 1943 2075 NQVMPKTGLLIIVIA 1944 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESEFQAAI 1946 2077 PRMFPDLESEFQAAI 1947 2079 QDFPVIFSKASEYL 1949 2080 QDLVQENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2081 QLVFGIEVVEVVPIS 1951 2082 RALIETSYVKYLHHT 1951 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2084 RKLLMQDLVQENYLE 1955 2085 STLVEVTLGEVPAA 1955 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLIIVLAIIAIEG 1956 2087 VFGIEVVEVPISHL 11977 2089 VFGIEVVPISHLXILVTC 1958 2090 VFGIEVVPISHLXILVTCLG 1960 2091 VVPISHLYILVTCLG 1960 2093 YEFLWGPRALIETSY 1963 | 2074 MVELVHFLLKYRAR 1943 2075 NQVMPKTGLLIIVIA 1944 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKMVELVHFL 1947 2079 QDFPVIFSKASEYL 1949 2080 QDLVQENYLEYRQVP 1950 2081 REPVTKAEMLESVLR 1951 2082 RALLETSYWKJLHT 1951 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2084 RKLLMQDLVQENYLE 1955 2086 SSTLVEYTGESVBA 1955 2087 YGLVHFLLKYRARE 1957 2089 VEJVHFLLKYRARE 1957 2090 VFGIEVVEVPISHL 11VTC 1958 2090 VFGIEVVEVPISHL 2091 2091 VVPISHLYILVTCG 1960 2092 YEFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1964 2095 YEFLWGPRALIETSY 1963 | PAA | 2073 | LVEVTLGEVPAADSP | 1942 | | | | | |
| 2075 NQVMPKTGLLIIVIA 1944 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKMVELVHFL 1947 2080 QDLVQENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2081 QLVFGIEVVEVVPIS 1951 2082 RALIETSYVKVLHHT 1951 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2084 RKLLMQDLVQENYLE 1953 2085 SHLYTLVTCLGLSYD 1954 2086 SSTLVEYTLGEVPAA 1955 2087 TGLLIIVLAIAIEG 1956 2087 VELVHFLLLKYRARE 1955 2090 VFGIEVVEVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2093 VFELWGPRALIETSY 1963 2094 YFILVTCLGLSYDGLL 1963 | 2075 NQVMPKTGLLIIVIA 1944 2076 PRKLLMQDLVQENYL 1945 2077 PRMFPDLESERQAAI 1946 2078 QAAISRKMVELVHFL 1947 2080 QDLVQENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2082 RALIETSYVKVLHHT 1951 2082 RALIETSYVKVLHHT 1951 2083 REPYTKAENLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2085 SHLYTLVTCLGLSVD 1954 2086 STLVTLVTCLGLSVD 1954 2087 TGLLIIVLAIIAIEG 1956 2087 TGLLIIVLAIIAIEG 1956 2080 VELVHFLLLKYRARE 1957 2090 VFGIEVVEVVPISHL 1959 2091 VVPPISHLYILVTCLG 1960 2092 VEELWGPRALIETSY 1962 2093 YEFLWGPRALIETSY 1963 2094 YTLVTCLGLSYDGLL 1964 2095 YPPLHERALREGEE- 1964 | LKY | 2074 | MVELVHFLLLKYRAR | 1943 | | | | | |
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| 2077 PRMFPDLESERQAAI 1946 2078 QAAISRKMVELVHFL 1947 2079 QDFFPVIFSRASEYL 1948 2080 QLVGEVVEVRPR 1949 2081 QLVGEVVEVRPR 1950 2081 RALIETSYVKYLHFT 1951 2083 REPVTKAEMLESVLR 1952 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2085 STLLVLGLSVD 1954 2086 STLVTLGEVAA 1955 2087 TGLLINYAIARG 1955 2088 VELVHFLLKYRARE 1957 2089 VELVHFLLKYRARE 1957 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTC 1958 2091 VVPISHLYILVTCLG 1960 2093 YEFLWGPRALIETSY 1963 | 2077 PRMFPDLESEFQAAI 1946 2078 QAAISRKMVELVHFL 1947 2079 QDLVQENYTEYRQVP 1949 2081 QDLVQENYEYRGVP 1949 2081 QLVFGIEVVEVVPIS 1950 2083 REPVTKAEMLESVLR 1951 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2085 SSTLVEVTLGESVD 1954 2086 SSTLVEVTLGEVAA 1955 2087 TGLLINTAIARG 1955 2087 VELVHFLLKYRARE 1957 2089 VELVHFLLKYRARE 1957 2090 VFGIEVVEVPISHL YILVTCLG 1960 2090 VFGIEVVEVPISHL YILVTCLG 1960 2091 YEFLWGPRALIETSY 1963 2093 YEFLWGPRALIETSY 1963 2094 YILVTCLGLSYDGLL 1964 | LVOF | 2076 | PRKI I MODI VOENYI. | 1945 | | | | | |
| 2079 QAAINEELLEYRANDEL VHFL 2079 QDFFPVIFSKASEYL 2080 QDLVQENYLEYRQVP 2081 QLVFGIEVVEVVPIS 2082 RALIETSYVKYLHHT 2083 REPVTKAEMLESVLR 1951 2084 RKLLMQDLVQENYLE 2085 SHLYLTVTCLGLSYD 2086 SSTLVEVTLGEVPAA 2087 TGLLIIVLAIIAIEG 2087 TGLLIIVLAIIAIEG 2087 VFGIEVVPISHL 1955 2089 VFGIEVVPISHLYILVTCLG 2090 VFGIEVVPISHLYILVTCLG 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2094 YILVTCLGLSYDGLL 2095 YEFLWGPRALIETSY 2095 YEFLWGPRALIETSY 2096 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YILVTCLGLSYDGLL 2097 YEFLWGPRALIETSY 2097 YEFLWGPRALIETSY 2097 YEFLWGPRALIETSY | 2079 QAAINELLINGERY 1947 2079 QDFFPVIFSKASEYL 1948 2080 QDLVQENYLEYRQVP 1949 2081 QLVFGIEVVEVVPIS 1950 2082 RALIETSYVKYLHHT 1951 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2084 RKLLMQDLVQENYLE 1953 2085 SHLYTUTCLGLSYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLINLAIAIEG 1956 2080 VELVHFLLKYRARE 1957 2090 VFGIEVVPISHLYILVTC 1959 2091 VVPISHLYILVTCLG 1960 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2094 YILVTCLGLSYDGLL 1964 | ביי | 7000 | PRMEPNI ESEENAAI | 1046 | | | | | |
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| 2082 RALIETSYVKVLHHT 1951 2083 REPYTKAENLESYLR 1952 2084 RKLIMQDLVQENYLE 1953 2085 SHLYILVTCLGLSYD 1954 2086 STLYTUYTCLGLSYD 1956 2087 TGLIIVLAIIAIEG 1956 2088 VELVHFLLLKYRARE 1957 2090 VFGIEVVEVPISHLY 11 1958 2090 VFGIEVVEVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 | 2082 RALIETSYVKVLHHT 1951 2083 REPVTRAENLESYLR 1952 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGLSYD 1954 2086 SSTLVETLGEVRAA 1955 2087 TGLLIIVLAIIAIEG 1956 2088 VELVHFLLLKYRARE 1957 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 YFFLWGPRALIETSY 1963 2095 YFFLWGPRALIETSY 1963 | EV | 2081 | QLVFGIEVVEVVPIS | 1950 | | | | | |
| 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2085 SHLYTLVTCLGLSYD 1954 2086 SSTLVETLGEVPAA 1955 2087 TGLLINVLAIREG 1956 2088 VELVHFLLLKYRARE 1957 2089 VELVPISHLYILVTC 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1953 | 2083 REPVTKAEMLESVLR 1952 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGLSYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLINTALIARE 1957 2089 VELVHFLLKYRARE 1957 2090 VFGIEVVEVPISHLYILVTC 1958 2090 VFGIEVVEVPISHLYILVTC 1960 2091 VEFLWGPRALLETSY 1960 2092 YEFLWGPRALLETSY 1960 2094 YILVTCLGLSYDGLL 1963 2095 YFFLWGPRALLETSY 1963 | XVI. | 2082 | RALIETSYVKVLHHT | 1921 | | | | | |
| 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGLSYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLIIVLAIIAIEG 1955 2087 VELVPIFILLKYRARE 1957 2089 VELVPIFILLKYRARE 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1953 | 2084 RKLLMQDLVQENYLE 1953 2085 SHLYILVTCLGLSYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLIIIVLAIIAIEG 1956 2089 VELVPISHLKYRARE 1957 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 YPPLHERALREGEE- 1964 | MI EC | 2083 | REPUTK A FMI FSVI R | 1952 | | | | | |
| 2085 SHLYUTCIGLSYD 1954 2086 SSTLVEVTLGEVPAA 1955 2087 TGLLIIVLAIAIEG 1955 2089 VELVHFILLKYRARE 1957 2090 VFGIEVVPISHLYILVTC 2090 VFGIEVVPEVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2093 YEFLWGPRALIETSY 1962 2094 YTILVTCLGLSYDGLL 1953 | 2085 SHLYUTCIGISYD 1954 2086 SSTLVEVTLGEVPA 1955 2087 TGLLIIVLAIAIEG 1955 2088 VELVHFLLLKYRARE 1957 2099 VFGIEVVEVPISHLYILVTC 1959 2091 VVPISHLYILVTC 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 YPPLHERALREGEE- 1964 | 700 | 2007 | PVI I MODI VOENVI E | 1953 | | | | | |
| 2085 STILLUTGEVRAA 1955 2086 STILLUTALIARG 2087 TGLLIIVLAIIARG 1956 2088 VELVHFLLLKYRARE 1957 2090 VFGIEVVEVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 | 2085 STILLUTGEVTA 1955 2086 STILLUTALIAIEG 2087 TGLLIIVLAIIAIEG 2089 VELVHFLLLKYRARE 1957 2090 VFGIEVVEVPISHL 11VTC 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 YPPLHERALREGEE- 1964 | | 2007 | 22 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 7501 | | | | | |
| 2085 SSILVEVILGEVRAN 1955 2087 TGLLIIVLAIIAIEG 1956 2088 VELVHFILLKYRARE 1957 2089 VEVPISHLYILVTC 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGIL 1953 | 2080 SSLLVEVILGEVTAA 1955 2087 TGLLIIVLAILAEG 2088 VELVHFLLKYRARE 1957 2090 VFGIEVVEVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 YPPLHERALREGEE- 1964 | 75 | 7007 | SOLITE VICEOUS IS | 300 | | | | | |
| 2087 TGLLIIVLAIIAEG 2088 VELVHFILLKYRARE 1955 2089 VEVPISHLYILVTC 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGIL 1963 | 2087 TGLLIIVLAIIAEG 2088 VELVHFILLKYRARE 1955 2089 VEVPISHLYILVTC 1958 2090 VFGIEVVEVVPISHL 1959 2091 VVPISHLYILVTCLG 1960 2092 WEELSMLEVFEGRED 1961 2093 YEFLWGPRALIETSY 1962 2094 YILVTCLGLSYDGLL 1963 2095 YPPLHERALREGEE- 1964 | 25. | 2080 | SSILVEVILGEVRAA | 666 | | | | | |
| 2088 VELVHFLLKYRARE 2089 VEVVPISHLYILVTC 2090 VFGIEVVEVPISHL 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 / YILVTCLGLSYDGLL | 2088 VELVHFLLKYRARE 2089 VEVVPISHLYILVTC 2090 VFGIEVVEVPISHL 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2095 YPPLHERALREGEE | | 2087 | TGLLIIVLAIIAIEG | 926 | | -0.0011 | | | |
| 2089 VEVVPISHLYILVTC 2090 VFGIEVVEVVPISHL 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2004 / YILVTCGLSYDGLL | 2089 VEVVPISHLYILVTC 2090 VFGIEVVEVVPISHL 2091 VVPISHLYILVTCG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2095 YPPLHERALREGEE | KYR | 2088 | VELVHFLLLKYRARE | 1957 | | | | | |
| 2090 VFGIEVVEVVPISHL 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 / YILVTCGLSYDGLL | 2090 VFGIEVVEVVPISHL 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2095 YPPLHERALREGEE- | YIL | 2089 | VEVVPISHLYILVTC | 1958 | | | | | |
| 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 / YILVTCLGLSYDGIL | 2091 VVPISHLYILVTCLG 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2095 YPPLHERALREGEE- | <u> </u> | 2090 | VFGIEVVEVVPISHL | 1959 | | | | | |
| 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSVDGLL | 2092 WEELSMLEVFEGRED 2093 YEFLWGPRALIETSY 2094 YILVTCLGLSYDGLL 2095 YPPLHERALREGEE- | 5 | 1900 | VVPISHI VII VTCI G | 1960 | | | | | |
| 2093 YEFUWGRALIETSY 2094 YILVTCLGLSYDGLL | 2093 YEFUNGPRALIETSY 2094 YILVTCLGLSYDGLL 2095 YPPUHERALREGEE- | 200 | 2002 | WEEL SMI EVERGRED | 1961 | | | | | |
| 2094 / YILVICLGLSYDGLL | 2094 YILYTCLGLSYDGLL 2095 YPPLHERALREGEE- | 2: | 7007 | WEELSIMILE VICTOR | 1061 | | | | | |
| 2094 / YILVICLGLATOULL | 2094 / YILVICLGESTEGEL 2095 / YPPLHERALREGEE- 1 | Lie Sign | 7060 | i Erch Gracies s | 706 | | | | | |
| | 2095 / YPPCHEKALKEGEE- | O.S. | 7 5002 | YILVICLGESTUGEE | 666 | | | | | |

| | DR5w12 | | | | | | | |
|--|-----------------------------------|------------------------------------|---|---|----------|-------|--|---------|
| | DR5w11 | | | | | | | |
| | DR4w4 DR4w15 DR5w11 | | | | | | | |
| , Data | DR4w4 | | | | | | | |
| th Binding | DR3 | | | | J 10 | | | |
| Mage 2 DR Super Motif Peptides with Binding Data | DR2w81 DR2w282 | | | | TO SUPER | | | |
| per Motif 1 | | | | | 2 | | | |
| 2 DR Su | DR1 | | | | | | | |
| Mage | Position | 260 285 | | | | | | |
| Table XIX A | Exemplary SeqID Num | 1965 1966 | 6 | _ | | | | |
| Tabl | Exemplary Sequence | YROVPGSDPACYEFL YVKVLHHTLKIGGEP | | | | , | | // \ |
| | Core SeqID Exemplary Num Sequence | 2096 | | | | | | |
| | Core Sequence | VPGSDPACY VLHHTLKIG | | | | | | |



| | DR5w12 | | | | | | | | | | | | | | | | | | | | - | | | | | | | 1 |
|--|------------------------|--|--|-------------------------------------|------------------------------------|-----------------|-------------------------------------|-----------------|-----------------|-----------------|----------------|------------------------------------|-----------------|------------------------|----------------|-----------------------------------|-----------------------------------|-------------------------|--------------------------|----------------|------------------------|-----------------|----------------|------------------------------------|------------------------------------|------------------------------------|------------------------------------|----|
| | DR5w11 | | | | 0.0310 | | | | | | -0.0008 | | | | | -0.0005 | | 0.0650 | -0.0005 | | | | | | | | | |
| | DR4w15 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | DR4w4 | -0.0008 | -0.0032 | | 0.0590 | | | 0.0110 | 0.000 | 700.0 | -0.0055 | 80000 | | | -0.0008 | -0.0032 | -0.0032 | 0.1100 | 0.0240 | | | | | | | | | |
| e distriction of the second | DR3 | | -0.0025 | 0.000 | 0.0059 | | | | | | 1.8000 | | | | | 0.0021 | | 9000'0 | 9000'0 | 0.0150 | 0.000 | | | | | | | |
| iiith Din | DR2w2ß2 | | | | 1.1000 | | | | | | -0.0010 | | | | | 0.0013 | | 0.0300 | -0.0007 | | | | | | | | | |
| tif Dontido | DR2w81 | | | | 0.3100 | | | | | | 0.0057 | | | | | 0.0020 | | 0.0030 | 0.0170 | | | | | | | | | |
| Mane 2 DD Curar Madif Dantidas with Dinding Date | DRI | 0.0045 0.0330 | -0.0003 | | 1.9000 | | | 0.0110 | 0.000 | 77000 | 0.0003 | 0 0043 | | | 0.0026 | 0.0250 | 0.0440 | 0.1100 | 0.0510 | | | | | | | | - | |
| Maga 1 DI | Position | 75 T16 | 183 189 50 50 50 50 50 50 50 50 50 50 50 50 50 | 322 | 255 104 | 49 | 149 | 1 <u>7</u> 1 | 202 | 120 | 99.2 | 134 | 245 | វុដុ | 503 | <u> </u> | 47 195 | 4 6 | 150 | 250 | 146 | 129 | ‡ <u>2</u> 2 | 163 | 142 224 | 271 303 | 260 285 | |
| Toble VIV D | Exemplary SeqID Num | 1967 1968 1969 | 1970 1971 | 1973 1974 | 1975 | 1977 | 1979 | 1981 | 1983 | 1985 | 1987 | 1989 | 66.5 | 661 | 566 | 986 1997 | 866 6 | 2000 2000 1000 | 2002 | 2004 | 2006 | 2008 | 2010 | 2012 | 2013 2014 | 2015 2016 | 2017 2018 | • |
| - 44°F | Exemplary Sequence | AELVHFLLKYRARE AGLLIIVLAIIAREG ALGLVGAQAPATEEQ | CLGLSYDGLLGDNQI DGLLGDNQIMPKAGL | SELWGPRALVETSYV SKIWEELSVLEVFEG | ENYLEYRQVPGSDPA ESEFQAALSRKVAEL | SVTLGEVPAAESPDP | PVIFSKASSSLOLV FFAI GI VGAOAPATF | SHLYIFATCLGLSYD | SLLIIVLAIIAREGD | HELLLKYRAREPUTK | ELMEVDPIGHLYIF | GALTIFATCLOLS T CAEMLGSVVGNWQYF | CKLLTQHFVQENYLE | GLVGAQAPATEEQE | LIIVLAIIAREGDC | LKY KAKEPVIKAEM QLVFGIELMEVDPI | VEVTLGEVPAAESP VQIMPKAGLLIIVLA | WQYFFPVIFSKASS | VIFSKASSSLQLVF | HFVQENYLEYRQVP | YFFPVIFSKASSSL | CEPVTKAEMLGSVVG | AELVIFILLKYRAR | ADPIGHLYIFAICLG AFGIELMEVDPIGHL | /GNWQYFFPVIFSKA WEELSVLEVFEGRED | YEFLWGPRALVETSY YPPLHEWVLREGEE- | YRQVPGSDPACYEFL YVKVLHHMVKISGGP | |
| | Core SeqID E | | 2101 | | | | | | | | | 2120 | | | | | | 2131 | | | | | | | ٠. | | 2148 | .1 |
| | Core | VHFLLLKYR LIIVLAIIA LVGAQAPAT | LSYDGLLGD LGDNQIMPK | WGPRALVET WGPRALVET WEELSVLEV | LEYRQVPGS FOAALSRKV | LGEVPAAES | IFSKASSSL I GI VGAOAP | YIFATCLGL | IIVLAIIAR | LLKYRAREP | MEVDPIGHL | MLGSVVGNW | LTQHFVQEN | VEARESFUR VGAQAPATE | VLAIIARE | YKAKEPVIK | VTLGEVPAA MPKAGLLII | YFFPVIFSK FPNI FSFFO | FSKASSSLQ I SRKVAFI V | VQENYLEYR | FPVIFSKAS VETSYVKVI | VTKAEMLGS | LVEVILGEV | IGHL YIFAT IELMEVDPI | WQYFFPVIF LSVLEVFEG | LWGPRALVE LHEWVLREG | VPGSDPACY VLHHMVKJS | |

SOOF SE

| | DRw53 | | | v | | | | | | | | | | | | | | | | | | | | | | | | | |
|--|------------------------|--|--|------------------------------------|-----------------|---|-------------------------|-----------------|------------------------------------|------------------------------------|---------------------------------|-------------------------------------|-----------------|------------------------------------|-----------------|-------------------------------------|---------------------------------------|--------------------------------------|-----------------|-----------------|------------------------------------|--|-----------------|------------------------|-----------------|-----------------|------------------------------------|------------------------------------|---|
| | DR9 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ding Data | DR8w2 | | | | 0.0430 | | | | | | 0.0130 | | | | | -0.0004 | | 0.2200 | 0.0038 | | | | | | | | | | |
| des with Bin | DR7 | -0.0026 | -0.0011 | | 0.7400 | | 3000 | 0.0023 | -0.0018 | | 0.0027 | 11000 | 100.0 | | -0.0018 | 0.0970 | 1100.0 | 0.0560 | 0.0890 | | | | | | | | | | |
| r Motif Pepti | DR6w19 | | | | 0.0005 | | | | | | 0.0130 | | | | | 0.0004 | | -0.0003 | 0.0240 | | | | | | | | | | |
| Mage 3 DR Super Motif Peptides with Binding Data | Exemplary SeqID Num | 1967 | 1970 1971 1971 | 1973 | 6761 9761 | 1978 | 1980 | 1982 | 1983 1984 | 1985 1986 | 1987 | 1989 | 1661 | 1992 1993 | 1995 | 1996 1997 | 1998 | 2000 | 2002 | 2003 | 2005 2006 | 2007 | 2009 2009 | 2010 2011 | 2012 | 2013 | 2015 2016 | 2017 2018 | « |
| Table XIX B | Exemplary Sequence | AELVHFLLLKYRARE AGLLIVLAIIAREG ALGLVGAQAPATEEQ | CLULS Y LUCLLUDNO! DGLLGDNQIMPKAGL FEKIWEE! SVI EVFF | EFLWGPRALVETSYV EKIWEELSVLEVFEG | ESEFQAALSRKVAEL | EVILGEVPAAESPDP FFPVIFSKASSSLQL FPVIFSVASSSI OI V | GEALGLYGAQAPATE | GIELMEVDPIGHLYI | GLLIIVLAIIAKEGD GPHISYPPLHEWVLR | HFLLLKYRAREPVTK HLYIFATCLGLSYDG | IELMEVDPIGHLYIF IGHLYIFATCLGLSY | KAEMLGSVVGNWQYF KAGI LIVI AIIARE | KKLLTQHFVQENYLE | LGEVPAAESPDPPQS LGLVGAQAPATEEQE | LLIIVLAIIAREGDC | LLK YRAREPVTKAEM LQLVFGIELMEVDPI | LVEVTLGEVPAAESP NOIMPKAGI I IIVI A | NWQYFFPVIFSKASS PCTEPNI FSFEOA AT | PVIFSKASSSLQLVF | QHFVQENYLEYRQVP | QLVFGIELMEVDPIG OYFFPVIFSKASSSL | RALVETSYVKVLHHM DEDVITY A EMI CSYVG | SSTLVEVTLGEVPAA | VAELVHFLLLKYRAR | VFGIELMEVDPIGHL | WEELSVLEVFEGRED | YEFLWGFKALVEISY YPPLHEWVLREGEE- | YRQVPGSDPACYEFL YVKVLHHMVKISGGP | |
| | Core SeqID Num | 2098 2099 2100 | 2102 2103 | 2104 | 2107 | 2109 | 2112 | 2113 | 2115 | 2116 | 2118 | 2120 | 2122 | 2124 | 2126 | 2128 | 2129 | 2131 | 2133 | 2135 | 2137 | 2138 | 2140 | 2141 | 2143 | 2145 | 2147 | 2148 | _ |
| | Core Sequence | VHFLLLKYR LIIVLAIIA LVGAQAPAT | LST DOLLOD LGDNQIMPK IWEELSVLE | WGPRALVET WEELSVLEV | FOAALSRKV | LUEVFARES VIFSKASSS IFSKASSS | LGLVGAQAP VIFATCI GI | LMEVDPIGH | IIVLAIIAK ISYPPLHEW | LLKYRAREP IFATCLGLS | MEVDPIGHL LYIFATCLG | MLGSVVGNW | LTQHFVQEN | VFARESFUR VGAQAPATE | IVLAIIARE | YKAKEPVIK VFGIELMEV | VTLGEVPAA MPKAGLLII | YFFPVIFSK FPDI ESEEO | FSKASSSLQ | VQENYLEYR | FOIELMEVD | VETSYVKVL VTK A EMI GS | LVEVTLGEV | LVHFLLLKY IGHLYIFAT | IELMEVDPI | LSVLEVFEG | LWGPKALVE LHEWVLREG | VPGSDPACY VLHHMVKIS | |

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Carrie 155 156 (")

155/1860

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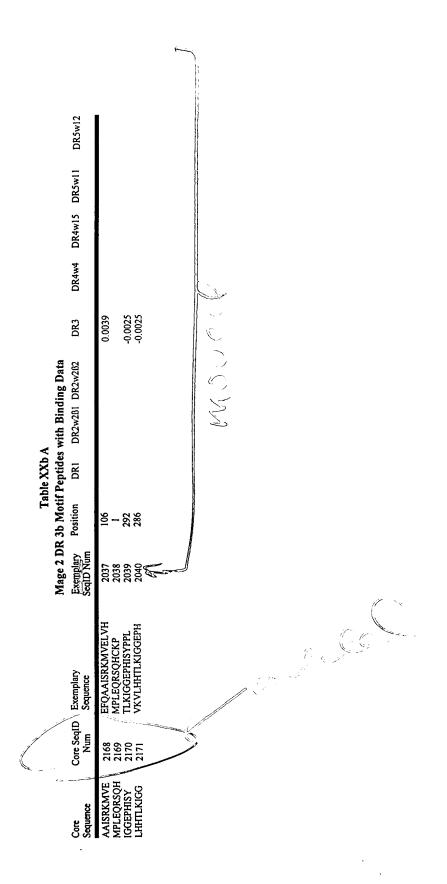
Carried State of the Carried S

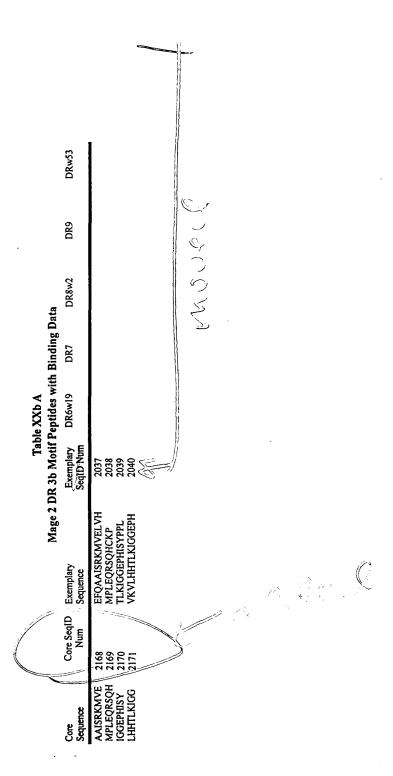
| | | |); }; }; |
|-------------|---|------------------------|--|
| | | DR5w12 | |
| | | DR4w15 DR5w11 | |
| | Mage 2 DR 3a Motif Peptides with Binding Data | DR4w15 | `· |
| Table XXa A | | DR4w4 | |
| | | DR3 | 0.1400 0.0130 0.0033 0.0039 0.0890 0.0890 0.0190 0.0072 0.1500 0.0270 |
| | | DR2w281 DR2w282 | |
| | | DR2w2B1 | |
| | | DR1 | |
| | | Position | 183 220 200 245 245 161 188 188 |
| | | Exemplary SeqID Num | 2019 2020 2021 2021 2023 2024 2025 2027 2027 2028 |
| 1 | | Exemplary Sequence | CLGLSYDGLLGDNOV EEKIWEELSMLEVFE FPDLESEFOAAISRK GPRMFPDLESEFOAA IGHGGDCAPEEKIW LAIIAIGGDCAPEEKIW LAIIAIGGDCAPEEKIW OLVFGIEVVEVVPIS RKLLMODLVOENYLEYROV OLVFGIEVLGDNOVMFKTG |
| | | Core SeqID Num | 2150 2151 2153 2153 2153 2153 2153 2153 2153 |
| | 4 | Core | LSYDGILGD WEELSMLE LESEFQAAI MEPDLESEF MEDCAPE LVQENYLEY FGIEVVEVV LMQDLVQEN LLGDNQVMP |

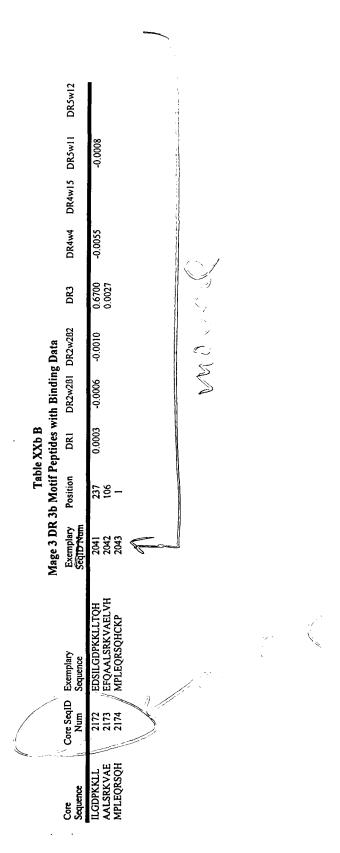
| | | DRw53 | |
|-------------|---|------------------------|---|
| | . Mage 2 DR 3a Motif Peptides with Binding Data | DR9 | |
| | | DR8w2 | |
| | | DR7 | . \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\ |
| Table XXa A | | DR6w19 | |
| | | Exemplary SeqID Num | 2019 2020 2021 2023 2023 2024 2025 2027 2027 2028 |
| | | Exemplary Sequence | CLGLSYDGLLGDNQV EEKIWEELSMLEVFE FPDLESEFQAAISRK GPRMFPDLESEFQAA IIAIEGDCAPEEKIW LAIIAIEGDCAPEEK MQDLVQENYLEYRQV QLVFGIEVVEVVPIS RKLLMQDLVQENYLE YDGLLGDNQVMPKTG |
| | | Core SeqID Num | 2150 2151 2152 2153 2154 2158 2158 2158 2158 |
| | | Core | LSYDGILGD IWEELSMLE LESEFQAAI MFPDLESEF IEGDCAPEE IAGEOVELY LVQENYLEY FGIEVVEVY LLGDNQVMP |

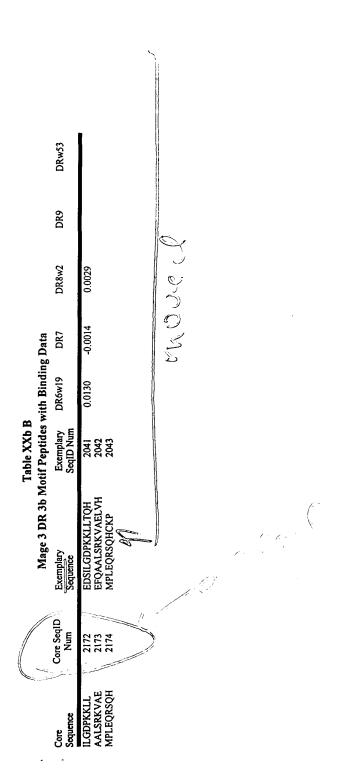
| | | | | 7. | | | | |
|-------------|---|------------------------|---|-----|---|--------------|-------|--|
| | ; | DR5w12 | | 1 | | | | |
| | ; | DR4w15 DR5w11 | -0.0008 | | | | | |
| | | DR4w15 | | | | | | |
| | | DR4w4 | -0.0055 | | | | | |
| | | DR3 | -0.0025 0.0058 0.0026 1.8000 -0.0025 0.0150 0.2800 | | | | | |
| | Mage 3 DR 3a Motif Peptides with Binding Data | DR2w2l31 DR2w2l32 | -0.0010 | | , | <u>\$</u> | | |
| Table XXa B | des with B | DR2w2B1 | 0.0057 | | | | | |
| | lotif Pepti | DRI | 0.0003 | | | | | |
| | 3 DR 3a M | Position | 183 220 100 166 208 161 188 | | | | | |
| | Mage 3 | Exemplary SeqID Num | 2029 2030 2031 2032 2033 2034 2035 2036 | (ها | | | | |
| | | | CLGLSYDGLLGDNQI EEKIWEELSVLEVFE FPDLESEFQAALSRK IELMEVDPIGHLYIF LAILAREGDCAPEEK QL VFGIELMEVDPIG TQHFVQENYLEYRQV YDGLLGDNQIMPKAG | 1 | | P ()) | K. G. | |
| | (| Core SeqI Num | 2160 2161 2162 2163 2164 2165 2165 2165 | |) | | | |
| | , | Core | LSYDGLLGD WEELSVLE LESEFQAAL MEVDPIGHL IAREGDCAP FGIELMEVD FVQENYLEY LLGDNQIMP | | | | | |

| | DRw53 | ĺ | | | |
|-------------|--|--|---------|-------|------|
| | DR | | | | |
| | DR9 | | | | |
| | DR8w2 | 0.0130 | | | |
| | ata DR7 | 0.0027 | S O O W | | |
| : ; | Binding D DR6w19 | 0.0130 | 2 | | |
| Table XXa B | Feptides with Exemplary SeqID Num | 2029 2030 2031 2032 2034 2035 2036 | | | |
| T ST COLOR | Mage 5 DK 3a Motif Peptides with Binding Data Exemplary Exemplary DR6w19 Sequence Sequence | CLGLSYDGLLGDNQI EEKIWEELSVLEVFE FPDLESEFQAALSRK IELMEVDPIGHLYIF LAIIAREGDCAPEEK QLYFGIELMEVDPIG TQHFVQENYLEYRQV YDGLLGDNQIMFKAG | Find? | J. Š. | GQ X |
| | Core SeqID Num | 2160 2161 2163 2163 2164 2165 2165 2167 | | | |
| | Core Sequence | LSYDGLLGD IWEELSVLE LESEFOAAL MEVDPIGHL IAREGDCAP FGIELMEVD FVOENYLEY | | | |









100000

Table XXII. A2 supermotif analogs

| | | 1 | / | | | | | | |
|---------------|----|-----------|------------------|--------------|--------------|--------------|--------------|--------------|---------------------------------|
| Source | AA | Sequence | SEQ ID NO: | A*0201 nM | A*0202 nM | A*0203 nM | A*0206 nM | A*6802 nM | No. A2 Alleles Crossbound |
| MAGE3.112 | 6 | KVAELVHFL | 2214 | 69 | 29 | 14 | 168 | 17 | 5 |
| MAGE3.112L2 | 6 | KLAELVHFL | 2215 | 70 | 0.9 | 5.9 | 12 | 400 | S |
| MAGE3.112M2 | 6 | KMAELVHFL | 2216 | 24 | 6.7 | 7.7 | 79 | 286 | ν, |
| MAGE3.112L2V9 | 6 | KLAELVHFV | 2217 | 14 | 13 | 22 | 15 | 73 | S |
| MAGE3.112M2V9 | 6 | KMAELVHFV | 2218 | 26 | 17 | 46 | 39 | 170 | 5 |
| MAGE3.220 | 6 | KIWEELSVL | 2219 | 333 | 391 | 2381 | 308 | : | 3 |
| MAGE3.220L2V9 | 6 | KLWEELSVV | 2220 | | 165 | 20 | 15 | 1 | 4 |
| | | | | | | | | | |

-- indicates binding affinity =10,000nM.

Table XXIIA A01 Analog Peptides

| | | | , – | | |
|----------------|-----------|-------------|-----------------|---------------|-----------|
| <u>Peptide</u> | <u>AA</u> | Sequence | SEQ ID NO: | <u>Source</u> | A*0101 nM |
| 52.0026 | 8 | ATCLGLSY | 2221 | MAGE3.179 | 227.3 |
| 52.013 | 11 | VVEVVPISHLY | 2222 | MAGE2.166 | 125 |
| 52.0132 | 11 | TMNYPLWSQSY | 2223 | MAGE3.74 | 301.2 |
| 52.0133 | 11 | LMEVDPIGHLY | 2224 | MAGE3.166 | 3.3 |
| 57.0003 | 8 | VTDLGLSY | 2225 | MAGE2.179.D3 | 2.7 |
| 57.0029 | 9 | STFSTTINY | 2226 | MAGE2.69.T2 | 490.2 |
| 57.003 | 9 | MTDLVQENY | 2227 | MAGE2.247.T2 | · 0.8 |
| 57.0031 | 9 | STLPTTMNY | 2228 | MAGE3.69.T2 | 58.1 |
| 57.0032 | 9 | GTVVGNWQY | 2229 | MAGE3.137.T2 | 36.2 |
| 57.0033 | 9 | ETDPIGHLY | 2230 | MAGE3.168.T2 | 0.7 |
| 57.0034 | 9 | ITGGPHISY | " 2231 3 | MAGE3.293.T2 | 36.2 |
| 57.0119 | 10 | ATSFSTTINY | 2232 | MAGE2.68.T2 | 454.5 |
| 57.012 | 10 | ASDFSTTINY | 2233 | MAGE2.68.D3 | 25 |
| 57.0121 | 10 | LTQDLVQENY | 2234 | MAGE2.246.T2 | 58.1 |
| 57.0122 | 10 | ATSLPTTMNY | 2235 | MAGE3.68.T2 | 208.3 |
| 57.0123 | 10 | ASDLPTTMNY | 2236 | MAGE3.68.D3 | 2.6 |
| 57.0124 | 10 | LTDHFVQENY | 2237 | MAGE3.246.D3 | 2.3 |

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| _ | 5.7 | 6.7 | 14.5 | 61.5 | 26.7 | 1.7 | 0.5 | 156.9 | 30.8 | 15.4 | 13.8 | 42.1 | |
| A*3301 nM A*6801 nM | 9666.7 | | | | | | 13.2 | 580 | -290000 | 1160 | 32.2 | 2989.7 | |
| A*3101 nM | 3333.3 | 62.1 | 720 | 0006 | 236.8 | 2769.2 | 9 | 620.7 | 12857.1 | 128.6 | 94.7 | 857.1 | |
| X*1101 pM / | 8.2 | 6.3 | 76.9 | 96.8 | 375 | က | 2.6 | 1538.5 | 62.5 | 171.4 | 375 | 103.4 | |
| A*0301 nM A*1101 nM A*3101 nM | 20 | 57.9 | 261.9 | 305.6 | 440 | 24.4 | 35.5 | 687.5 | 392.9 | 36666.7 | 117 | 42.3 | |
| Source | MAGE2.69.V2K9 | MAGE2.69.V2R9 | MAGE2.73.V2 | MAGE2.73.V2K9 | MAGE2/3.116.R9 | MAGE3.138.V2 | MAGE3.138.V2R9 | MAGE2.237.R8 | MAGE2.277.V2 | MAGE2.277.V2R9 | MAGE2.299.V2 | MAGE2.299.V2K9 | |
| SEQ ID NO: | 2238 | 2239 | 2240 | 2241 | 2242 | 2243 | 2244 | \ 2245 | \ 2246 | 2247 | 2248 | 2249 | |
| | | | | | | | • | | | | | | |
| Seguence | SVFSTTINK | SVFSTTINR | TVINYTLWR | TVINYTLWK | LVHFLLLKR | YVFPVIFSK | YVFPVIFSR | SVFAHPRR | AVIETSYVK | AVIETSYVR | IVYPPLHER | IVYPPLHEK | |
| ₽ | თ | თ | თ | တ | တ | თ | တ | œ | တ | တ | တ | တ | |
| Peptide | 1371.63 | 1371.64 | 1371.65 | 1371.66 | 1371.68 | 1371.69 | 1371.7 | 1371.71 | 1371.72 | 1371.73 | 1371.74 | 1371.75 | · |

Table XXIIC A24 Analog Peptides

| | | | \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\ | | |
|----------------|----|-------------|--|-----------------|-------------|
| <u>Peptide</u> | AA | Sequence | SEQ ID NO: | <u>Source</u> | A*2401 |
| 52.0072 | 0 | LWGPRALI | 3350 | MAGE2.272 | · <u>nM</u> |
| | 8 | | 2250 | | 100 |
| 52.0073 | 8 | QYFFPVIF | 2251 | MAGE3.144 | 100 |
| 52.0078 | 8 | SYPPLHEW | 2252 | MAGE3.300 | 285.7 |
| 52.0102 | 10 | SYPPLHEWVL | 2253 | MAGE3.300 | 20.3 |
| 52.0166 | 11 | SFSTTINYTLW | 2254 | MAGE2.70 | 428.6 |
| 52.0167 | 11 | IFSKASEYLQL | 2255 | MAGE2.150 | 126.3 |
| 52.017 | 11 | IFSKASSSLQL | 2256 | MAGE3.150 | 131.9 |
| 52.0172 | 11 | IWEELSVLEVF | 2257 | MAGE3.221 | 461.5 |
| 57.006 | 9 | MYPDLESEF | 2258 | MAGE2.97.Y2 | 52.2 |
| 57.0061 | 9 | KYVELVHFF | 2259 | MAGE2.112.Y2F9 | 7.1 |
| 57.0062 | 9 | IYSKASEYF | 2260 | MAGE2.150.Y2F9 | 14.6 |
| 57.0063 | 9 | EYLQLVFGF | 2261 | MAGE2.156.F9 | 4 |
| 57.0064 | 9 | VYPKTGLLF | 2262 | MAGE2.195.Y2F9 | 5.5 |
| 57.0065 | 9 | TYPDLESEF | 2263 | MAGE3.97.Y2 | 218.2 |
| 57.0066 | 9 | NYQYFFPVF | 2264 | MAGE3.142.Y2F9 | 3.4 |
| 57.0067 | 9 | IYSKASSSF | 2265 | MAGE3.150.Y2F9 | 375 |
| 57.0068 | 9 | IYPKAGLLF | 2266 | MAGE3.195.Y2F9 | 9.2 |
| 57.0084 | 10 | SYSTTINYTF | 2267 | MAGE2.70.Y2F10 | 14.8 |
| 57.0085 | 10 | LYILVTCLGF | 2268 | MAGE2.175.F10 | 17.6 |
| 57.0086 | 10 | VYPKTGLLIF | 2269 | MAGE2.195.Y2F10 | 2.9 |
| 57.0087 | 10 | EYLWGPRALF | 2270 | MAGE2.270.Y2F10 | 10 |
| 57.0088 | 10 | SYVKVLHHTF | 2271 | MAGE2.282.F10 | 34.3 |
| 57.009 | 10 | NYQYFFPVIF | 2272 | MAGE3.142.Y2 | 22.6 |
| 57.0092 | 10 | LYIFATCLGF | 2273 | MAGE3.175.F10 | 10 |
| 57.0093 | 10 | IYPKAGLLIF | 2274 | MAGE3.195.Y2F10 | 1.2 |
| 57.0095 | 10 | SYPPLHEWVF | 2275 | MAGE3.300.F10 | 5.5 |
| | | | | | |

Table XXIII. Immunogenicity of A2 supermotif peptides

| | | |). | | | | | | | | |
|-----------|----|-------------|---------------|--------------|--------------|--------------|--------------|--------------|------------------------------|-------------------------------|------|
| Source | AA | Sequence | SEQ ID NO: | A*0201 nM | A*0202 nM | A*0203 nM | A*0206 nM | A*6802 nM | No. A2 Alleles Crossbound | CTL Wild-type ¹ | CTL |
| MAGE2.112 | 6 | KMVELVHFL | 2276 | 9.8 | 25 | 17 | 123 | 2353 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 10 | KMVELVHFLL | 2277 | 23 | 39 | 127 | 9.0 | 2667 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 11 | KMVELVHFLLL | 2278 | 5.0 | 45 | 63 | 109 | 7692 | 4 | 1/1 | 0/1 |
| MAGE2.153 | 6 | KASEYLQLV | 2279 | 152 | 116 | 17 | 185 | 4878 | 4 | 2/4 | 0/2 |
| MAGE2.157 | 10 | YLQLVFGIEV | 2280 | 20 | 165 | 345 | 370 | 9302 | 4 | 3/3 | 1/3 |
| MAGE2.160 | 10 | LVFGIEVVEV | 2281 | 357 | 20 | 43 | 28 | 8.0 | S | 4/4 | 0/3 |
| MAGE3.112 | 6 | KVAELVHFL | 2282 | 89 | 53 | 14 | 168 | 17 | 5 | 3/4 | 3/4 |
| MAGE3.112 | 10 | KVAELVHFLL | 2283 | 54 | 36 | 217 | 206 | 11 | 5 | 0/1 | 0/1 |
| MAGE3.159 | 11 | QLVFGIELMEV | 2284 | 7.9 | 74 | 217 | 185 | 267 | 5 | 3/3 | 1/32 |
| MAGE3.160 | 10 | LVFGIELMEV | 2285 | 59 | 20 | 7.7 | 28 | 14 | 5 | 4/4 | 1/42 |
| MAGE3.195 | 11 | IMPKAGLLIIV | 2286 | 70 | 226 | 14 | 176 | ۳, | 4 | 3/4 | 0/3 |
| MAGE3.220 | 6 | KIWEELSVL | 2287 | 357 | 391 | 2381 | 308 | ! | 3 | 3/4 | 0/3 |
| MAGE3.271 | 6 | FLWGPRALV | 2288 | 31 | 43 | 14 | 336 | 40 | \$ | 4/4 | 2/4 |
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1) Indicates the number of donors positive over the total number of donors tested.

2) A positive result was seen after the second restim. 3) -- indicates binding affinity =10,000nM.

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Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

| A. Class | A. Class I binding assays | ssays | | Rac | Radiolabeled peptide | |
|----------|---------------------------|---------|-----------------------|----------------------------|----------------------|------------|
| Species | Antigen | Allele | Cell line | Source | Sequence | SEQ ID NO: |
| Human | A1 | A*0101 | Steinlin | Hu. J chain 102-110 | YTAVVPLVY | 2289 |
| | A 2 | A*0201 | ጟ | HBVc 18-27 F6->Y | FLPSDYFPSV | 2290 |
| | 4 2 | A*0202 | P815 (transfected) | HBVc 18-27 F6->Y | FLPSDYFPSV | 2291 |
| | A 2 | A*0203 | FUN | HBVc 18-27 F6->Y | FLPSDYFPSV | 2292 |
| | A 2 | A*0206 | CLA | HBVc 18-27 F6->Y | FLPSDYFPSV | 2293 |
| | 4 2 | A*0207 | 721.221 (transfected) | HBVc 18-27 F6->Y | FLPSDYFPSV | 2294 |
| | A3 | | GM3107 | non-natural (A3CON1) | KVFPYALINK | 2295 |
| | A11 | | BVR | non-natural (A3CON1) | KVFPYALINK | 2296 |
| | A24 | A*2402 | KAS116 | non-natural (A24CON1) | AYIDNYNKF | 2297 |
| | A31 | A*3101 | SPACH | non-natural (A3CON1) | KVFPYALINK | 2298 |
| | A33 | A*3301 | LWAGS | non-natural (A3CON1) | KVFPYALINK | 2299 |
| | A28/68 | A*6801 | CIR | HBVc 141-151 T7->Y | STLPETYVVRR | 2300 |
| | A28/68 | A*6802 | AMAI | HBV pol 646-654 C4->A | FTQAGYPAL | 2301 |
| | B7 | B*0702 | GM3107 | A2 sigal seq. 5-13 (L7->Y) | APRTLVYLL | 2302 |
| | B8 | B*0801 | Steinlin | HIVgp 586-593 Y1->F, Q5->Y | FLKDYQLL | 2303 |
| | B27 | B*2705 | LG2 | R 60s | FRYNGLIHR | 2304 |
| | B35 | B*3501 | CIR, BVR | non-natural (B35CON2) | FPFKYAAAF | 2305 |
| | B35 | B*3502 | TISI | non-natural (B35CON2) | FPFKYAAAF | 2306 |
| | B35 | B*3503 | EHM | non-natural (B35CON2) | FPFKYAAAF | 2307 |
| | B44 | B*4403 | PITOUT | EF-1 G6->Y | AEMGKYSFY | 2308 |
| | B51 | | KAS116 | non-natural (B35CON2) | FPFKYAAAF | 2309 |
| | B53 | B*5301 | AMAI | non-natural (B35CON2) | FPFKYAAAF | 2310 |
| | B54 | B*5401 | KT3 | non-natural (B35CON2) | FPFKYAAAF | 2311 |
| | Cw4 | Cw*0401 | CIR | non-natural (C4CON1) | QYDDAVYKL | 2312 |
| | Cw6 | Cw*0602 | 721.221 transfected | non-natural (C6CON1) | YRHDGGNVL | 2313 |
| | Cw7 | Cw*0702 | 721.221 transfected | non-natural (C6CON1) | YRHDGGNVL | 2314 |
| Mouse | ρ | | EL4 | Adenovirus E1A P7->Y | SGPSNTYPEI | 2315 |
| | М _р | | EL4 | VSV NP 52-59 | RGYVFQGL | 2316 |
| | ρ _Q | | P815 | HIV-IIIB ENV G4->Y | RGPYRAFVTI | 2317 |
| | Kq | | P815 | non-natural (KdCON1) | KFNPMKTYI | 2318 |
| | $\Gamma^{\mathfrak{q}}$ | | P815 | HBVs 28-39 | IPQSLDSYWTSL | 2319 |
| | | | | | | |

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|----------------------|----------------------|--------------------|--------------------|--------------------|-------------------|-----------------------|------------------------|------------------------|------------------------|---|
| | | 1 | -: | - | Ã | F 224 17 | t.= _ | | | |
| 1007 | 2338 | 2339 | 2340 | 2341 | 2342 | 2343 | 2344 | 2345 | 2346 | |
| | YARFQSQTTLKQKT | YAHAAHAAHAAHAA | ҮАНААНААНААНАА | ҮАНААНААНААНАА | YNTDGSTDYGILQINSR | ХАНААНААНААНАА | ҮАНААНААНААН АА | YLEDARRKKAIYEKKK | YLEDARRKKAIYEKKK | |
| 1 CF 0 CO CO CO TO T | non-natural (717.01) | non-natural (ROIV) | non-natural (ROIV) | non-natural (ROIV) | HEL 46-61 | non-natural (ROIV) | non-natural (ROIV) | Lambda repressor 12-26 | Lambda repressor 12-26 | |
| TUTAL | L257.6 | PF | DB27.4 | A20 | CH-12 | LS102.9 | 91.7 | A20 | CH-12 | |
| TOTO COVID | DRB4*0101 | IQA1*0301/DQB1*030 | | | | | | | | |
| 2 | DR53 | DQ3.1 | ΙΑ _β | Ι¥q | ΙΑ ^k | ΙΑ³ | ΙΑ ^υ | E | EĚ | ï |

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| | | | | | Radiolabeled peptide | |
|---------|-----------------|--------------------|------------------|------------------------|----------------------|------------|
| Species | Antigen | Allele | Cell line | Source | Sequence | SEQ ID NO: |
| Human | DRI | DRB1*0101 | rg5 | HA Y307-319 | YPKYVKQNTLKLAT | 2320 |
| | DR2 | DRB1*1501 | L466.1 | MBP 88-102Y | VVHFFKNIVTPRTPPY | 2321 |
| | DR2 | DRB1*1601 | L242.5 | non-natural (760.16) | YAAFAAAKTAAAFA | 2322 |
| | DR3 | DRB1*0301 | MAT | MT 65kD Y3-13 | YKTIAFDEEARR | 2323 |
| | DR4w4 | DRB1*0401 | Preiss | non-natural (717.01) | YARFQSQTTLKQKT | 2324 |
| | DR4w10 | DRB1*0402 | YAR | non-natural (717.10) | YARFQRQTTLKAAA | 2325 |
| | DR4w14 | DRB1*0404 | BIN 40 | non-natural (717.01) | YARFQSQTTLKQKT | 2326 |
| | DR4w15 | DRB1*0405 | KT3 | non-natural (717.01) | YARFQSQTTLKQKT | 2327 |
| | DR7 | DRB1*0701 | Pitout | Tet. tox. 830-843 | QYIKANSKFIGITE | 2328 |
| | DR8 | DRB1*0802 | OLL | Tet. tox. 830-843 | QYIKANSKFIGITE | 2329 |
| | DR8 | DRB1*0803 | LUY | Tet. tox. 830-843 | QYIKANSKFIGITE | 2330 |
| | DR9 | DRB1*0901 | HID | Tet. tox. 830-843 | QYIKANSKFIGITE | 2331 |
| | DR11 | DRB1*1101 | Sweig | Tet. tox. 830-843 | QYIKANSKFIGITE | 2332 |
| | DR12 | DRB1*1201 | Herluf | unknown eluted peptide | EALIHQLKINPYVLS | 2333 |
| | DR13 | DRB1*1302 | H0301 | Tet. tox. 830-843 S->A | QYIKANAKFIGITE | 2334 |
| | DR51 | DRB5*0101 | GM3107 or L416.3 | Tet. tox. 830-843 | QYIKANAKFIGITE | 2335 |
| | DR51 | DRB5*0201 | L255.1 | HA 307-319 | PKYVKQNTLKLAT | 2336 |
| | DR52 | DRB3*0101 | MAT | Tet. tox. 830-843 | NGQIGNDPNRDIL | 2337 |
| | DR53 | DRB4*0101 | L257.6 | non-natural (717.01) | YARFQSQTTLKQKT | 2338 |
| | DQ3.1 | 1QA1*0301/DQB1*03C | PF | non-natural (ROIV) | YAHAAHAAHAAHAA | 2339 |
| Mouse | IA | | DB27.4 | non-natural (ROIV) | ҮАНААНААНААНАА | 2340 |
| | ΙΑ ^φ | | A20 | non-natural (ROIV) | ҮАНААНААНААНАА | 2341 |
| | ΙΑ ^k | | CH-12 | HEL 46-61 | YNTDGSTDYGILQINSR | 2342 |
| | ΙΑ | | LS102.9 | non-natural (ROIV) | ҮАНААНААНААНАА | 2343 |
| | ΙΑ ^u | | 91.7 | non-natural (ROIV) | ҮАНААНААНААНАА | 2344 |
| | IEq | | A20 | Lambda repressor 12-26 | YLEDARRKKAIYEKKK | 2345 |
| | 压 | | CH-12 | Lambda repressor 12-26 | YLEDARRKKAIYEKKK | 2346 |
| | | | | | | |

Table XXVI. Crossbinding data A2 supermotif peptides

| | | | 1 | | | | | | |
|------------|---|-------------|------------------|-------------------|--------------|--------------|--------------|--------------|------------------------------|
| Source | AA | Sequence | SEQ ID NO: | , A*0201 nM | A*0202 nM | A*0203 nM | A*0206 nM | A*6802 nM | No. A2 Alleles Crossbound |
| MAGE2.112 | 6 | KMVELVHFL | 2347 | 38 | 15 | 9.1 | 49 | 364 | 5 |
| MAGE2.112 | 10 | KMVELVHFLL | 2348 | 23 | 39 | 127 | 0.6 | 7997 | 4 |
| MAGE2.112 | 11 | KMVELVHFLLL | 2349 | 5.0 | 45 | 63 | 109 | 7692 | 4 |
| MAGE2.153 | 6 | KASEYLQLV | 2350 | 152 | 116 | 17 | 185 | 4878 | 4 |
| MAGE2.157 | 10 | YLQLVFGIEV | 2351 | 20 | 165 | 345 | 370 | 9302 | 4 |
| MAGE2.160 | 10 | LVFGIEVVEV | 2352 | 357 | 21 | 44 | 29 | 8.0 | 5 |
| MAGE2.220 | 6 | KIWEELSML | 2353 | 167 | 642 | 175 | 53 | 1 | 33 |
| MAGE2.271 | 6 | FLWGPRALI | 2354 | 238 | 96 | 137 | 1542 | 95 | 4 |
| MAGE2.277 | 10 | ALIETSYVKV | 2355 | 200 | 729 | 125 | 1947 | 3077 | 2 |
| MAGE2/3.44 | 10 | TLVEVTLGEV | 2356 | <i>L</i> 9 | 39 | 4.3 | 218 | 33 | 5 |
| MAGE3.112 | 6 | KVAELVHFL | 2357 | 89 | 29 | 14 | 168 | 17 | 5 |
| MAGE3.112 | 10 | KVAELVHFLL | 2358 | 54 | 36 | 217 | 506 | Ξ | 5 |
| MAGE3.159 | 11 | QLVFGIELMEV | 2359 | 7.9 | 74 | 217 | 185 | 797 | 5 |
| MAGE3.160 | 10 | LVFGIELMEV | 2360 | 53 | 20 | 7.7 | 29 | 14 | 5 |
| MAGE3.174 | Ξ | HLYIFATCLGL | 2361 | 99 | 741 | 692 | : | 4494 | 1 |
| MAGE3.176 | 6 | YIFATCLGL | 2362 | 185 | 45 | 37 | 1028 | 222 | 4 |
| MAGE3.195 | ======================================= | IMPKAGLLIIV | 2363 | 70 | 226 | 15 | 176 | : | 4 |
| MAGE3.220 | 6 | KIWEELSVL | 2364 | 333 | 391 | 2381 | 308 | : | 3 |
| MAGE3.271 | 6 | FLWGPRALV | 2365 | 31 | 43 | 14 | 336 | 40 | \$ |
| | | | | | | | | | |

-- indicates binding affinity =10,000nM.

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Table XXVII. Immunogenicity of A2 supermotif peptides

| | | | (1) (1) (1) | 10004 | 0000 | 7 | 7000 | 0007 | | 14.0 | į |
|-----------|----|-------------|-------------|--------------|--------------|---------------|---------------|--------------|------------------------------|-----------|-------|
| Source | ΑA | Sequence | SEC ID | A-0201 nM | A*0202 nM | A**0203 nM | A*'0200 nM | A-6802 nM | No. Az Alleles Crossbound | Vild-type | Tumor |
| MAGE2.112 | 6 | KMVELVHFL | 2366 | 8.6 | 25 | 17 | 123 | 2353 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 10 | KMVELVHFLL | 2367 | 23 | 39 | 127 | 9.0 | 7997 | 4 | 1/1 | 0/1 |
| MAGE2.112 | 11 | KMVELVHFLLL | 2368 | 5.0 | 45 | 63 | 109 | 7692 | 4 | 1/1 | 0/1 |
| MAGE2.153 | 6 | KASEYLQLV | 2369 | 152 | 116 | 17 | 185 | 4878 | 4 | 2/4 | 0/2 |
| MAGE2.157 | 10 | YLQLVFGIEV | 2370 | 20 | 165 | 345 | 370 | 9302 | 4 | 3/3 | 1/3 |
| MAGE2.160 | 10 | LVFGIEVVEV | 2371 | 357 | 70 | 43 | 28 | 8.0 | 5 | 4/4 | 0/3 |
| MAGE3.112 | 6 | KVAELVHFL | 2372 | 89 | 53 | 14 | 168 | 17 | 5 | 3/4 | 3/4 |
| MAGE3.112 | 10 | KVAELVHFLL | 2373 | 54 | 36 | 217 | 206 | Ξ | 5 | 0/1 | 0/1 |
| MAGE3.159 | 11 | QLVFGIELMEV | 2374 | 7.9 | 74 | 217 | 185 | 267 | 5 | 3/3 | 1/32 |
| MAGE3.160 | 10 | LVFGIELMEV | 2375 | 29 | 20 | 7.7 | 28 | 14 | 5 | 4/4 | 1/42 |
| MAGE3.195 | 11 | IMPKAGLLIIV | 2376 | 70 | 226 | 14 | 176 | ۳ ا | 4 | 3/4 | 0/3 |
| MAGE3.220 | 6 | KIWEELSVL | 2377 | 357 | 391 | 2381 | 308 | 1 | 3 | 3/4 | 0/3 |
| MAGE3.271 | 6 | FLWGPRALV | 2378 | 31 | 43 | 14 | 336 | 40 | 5 | 4/4 | 2/4 |
| | | | | 3 | | | | | | | |

Indicates the number of donors positive over the total number of donors tested.
 A positive result was seen after the second restim.
 - indicates binding affinity =10,000nM.

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Table XXVIII. DR supertype primary binding

| Peptide | DR147 Algo Sum | Sequence | SEQ ID NO: | Source | DR1 nM | DR4w4 nM | DR7 nM | DR147 Cross- binding |
|---------|----------------------|------------------------|---------------|------------|-----------|-------------|-----------|----------------------------|
| 39.0282 | 2 | LGEVPAADSPSPPHS | 2379 | MAGE2.50 | | | | 0 |
| 39.0283 | 3 | ESEFQAAISRKMVEL | 2380 | MAGE2.102 | 4.2 | 28 ļ | 49 | 3 |
| 39.0284 | 2 | GIEVVEVVPISHLYI | 2381 # | MAGE2.163 | 595 | 6429 | 278 | 2 |
| 39.0285 | 2 | DGLLGDNQVMPKTGL | 2382 | MAGE2.187 | | | | 0 |
| 39.0286 | 2 | NQVMPKTGLLIIVLA | 2383 | MAGE2.193 | 2632 | | | 0 |
| 39.0287 | 2 | KTGLLIIVLAIIAIE | 2384 | MAGE2.198 | 417 | 1216 | 862 | 2 |
| 39.0288 | 2 | TGLLIIVLAIIAIEG | 2385 | MAGE2.199 | 6250 | | | 0 |
| 39.0291 | 2 | GLLIIVLAIIAIEGD | 2386 | MAGE2.200 | 500 | | | 1 |
| 39.0292 | 3 | LLIIVLAIIAIEGDC | 2387 | MAGE2.201 | 581 | 3750 | 1923 | 1 |
| 39.0293 | 2 | LIIVLAIIAIEGDCA | 2388 | MAGE2.202 | 417 | 8824 | 2083 | 1 |
| 39.0294 | 2 | EPHISYPPLHERALR | 2389 | MAGE2.296 | | | | 0 |
| 39.0295 | 3 | ALGLVGAQAPATEEQ | 2390 | MAGE2/3.22 | 152 | | | 1 |
| 39.0296 | 2 | ESEFQAALSRKVAEL | 2391 | MAGE3.102 | 2.6 | 763 | 34 | 3 |
| 39.0297 | 2 | NWQYFFPVIFSKASS | 2392 | MAGE3.142 | 46 | 409 | 446 | 3 |
| 39.0298 | 3 | PVIFSKASSSLQLVF | 2393 | MAGE3.148 | 98 | 1875 | 281 | 2 |
| 39.0299 | 3 | LQLVFGIELMEVDPI | 2394 | MAGE3.158 | 200 | | 258 | 2 |
| 39.0300 | 3 | GHLYIFATCLGLSYD | 2395 | MAGE3.173 | 455 | 4091 | | 1 |
| 39.0301 | 2 | DGLLGDNQIMPKAGL | 2396 | MAGE3.187 | | | | 0 |
| 39.0302 | 2 | NQIMPKAGLLIIVLA | 2397 | MAGE3.193 | 114 | | | 1 |
| 39.0303 | 2 | KAGLLIIVLAIIARE | 2398 | MAGE3.198 | 1163 | | | 0 |
| 39.0304 | 2 | AGLLIIVLAIIAREG | 2399 | MAGE3.199 | 1111 | | >9615 | 0 |
| 39.0305 | 3 | LLIIVLAIIAREGDC | 2400 | MAGE3.201 | 1923 | | | 0 |
| 39.0306 | 2 | GPHISYPPLHEWVLR | 2401 | MAGE3.296 | 2273 | | | 0 |

⁻⁻ indicates binding affinity =10,000nM.

4

Table XXIX. DR supertype crossbinding

| Peptide | Sequence | SEQ ID NO: | Source | DR1 nM | DR4w4 nM | DR7 nM | DR2w2 β1 nM | DR2w2 β2 nM | DR6w1 9 nM | DR5w1 1 nM | DR8w2 nM | DR 147 Cross- binding | Broad Binding (5/8) |
|---------|-------------------------|---------------|-----------|-----------|-------------|-----------|----------------|----------------|---------------|---------------|-------------|-----------------------------|---------------------------|
| 39.0283 | 39.0283 ESEFQAAISRKMVEL | 2402 | MAGE2.102 | 4.2 | 281 | 49 | 147 | 20 | 522 | 741 | 1581 | 3 | 7 |
| 39.0284 | 39.0284 GIEVVEVVPISHLYI | 2403 | MAGE2.163 | 595 | 6429 | 278 | 1978 | : | 49 | : | 5506 | 7 | m |
| 39.0287 | KTGLLIIVLAIIAIE | 2404 | MAGE2.198 | 417 | 1216 | 862 | 2460 | 1 | 2333 | ; | ł | 7 | 7 |
| 39.0296 | ESEFQAALSRKVAEL | 2405 | MAGE3.102 | 5.6 | 763 | 34 | 59 | 18 | 2000 | 645 | 1140 | r | 9 |
| 39.0297 | NWQYFFPVIFSKASS | 2406 | MAGE3.142 | 46 | 409 | 446 | 3033 | <i>L</i> 99 | 1 | 308 | 223 | n | 9 |
| 39.0298 | | 2407 | MAGE3.148 | 86 | 1875 | 281 | 535 | ŀ | 146 | : | ; | 7 | 4 |
| 39.0299 | LQLVFGIELMEVDPI | 2408 | MAGE3.158 | 200 | ; | 258 | 4550 | ŀ | 8750 | : | ŀ | 2 | 7 |
| | | | | | | | | | | | | | |

-- indicates binding affinity =10,000nM.

180

Table XXX. DR3 binding

| | | | = | |
|---------|------------------------|---------------|-----------|-----------|
| Peptide | Sequence | SEQ ID NO: | Source | DR3 nM |
| 39.0384 | GPRMFPDLESEFQAA | 2409 | MAGE2.94 | 3371 |
| 39.0387 | FPDLESEFQAAISRK | 2410 | MAGE2.98 | |
| 39.0388 | EFQAAISRKMVELVH | 2411 | MAGE2.104 | |
| 39.0389 | QLVFGIEVVEVVPIS | 2412 | MAGE2.159 | |
| 39.0390 | CLGLSYDGLLGDNQV | 2413 | MAGE2.181 | 2143 |
| 39.0391 | YDGLLGDNQVMPKTG | 2414 | MAGE2.186 | |
| 39.0392 | LAIIAIEGDCAPEEK | 2415 | MAGE2.206 | |
| 39.0393 | IIAIEGDCAPEEKIW | 2416 | MAGE2.208 | 4546 |
| 39.0394 | EEKIWEELSMLEVFE | 2417 | MAGE2.218 | |
| 39.0395 | RKLLMQDLVQENYLE | 2418 | MAGE2.243 | 2000 |
| 39.0396 | MQDLVQENYLEYRQV | 2419/ | MAGE2.247 | 1500 |
| 39.0397 | VKVLHHTLKIGGEPH | 2420 | MAGE2.284 | |
| 39.0398 | TLKIGGEPHISYPPL | 2421 | MAGE2.290 | |
| 39.0399 | FPDLESEFQAALSRK | 2422 | MAGE3.98 | |
| 39.0400 | EFQAALSRKVAELVH | 2423 | MAGE3.104 | |
| 39.0401 | QLVFGIELMEVDPIG | 2424 | MAGE3.159 | |
| 39.0402 | IELMEVDPIGHLYIF | 2425 | MAGE3.164 | 167 |
| 39.0403 | CLGLSYDGLLGDNQI | 2426 | MAGE3.181 | |
| 39.0404 | YDGLLGDNQIMPKAG | 2427 | MAGE3.186 | |
| 39.0405 | LAIIAREGDCAPEEK | 2428 | MAGE3.206 | |
| 39.0406 | EEKIWEELSVLEVFE | 2429 | MAGE3.218 | |
| 39.0407 | EDSILGDPKKLLTQH | 2430 | MAGE3.235 | 448 |
| 39.0408 | TQHFVQENYLEYRQV | 2431 | MAGE3.247 | 1071 |

⁻⁻ indicates binding affinity =10,000nM.

Table XXXI. HTL Candidates

| l 4 | | | | | |
|-----------------------------|--|-------------------------|------------------------------|-----------------|------------------------------|
| DR3 Binder | 0 | 0 | 0 | _ | 1 |
| Broad Binding (5/8) | 7 | 9 | 9 | _ | 1 |
| DR 147 Cross- binding | 3 | 33 | n | 0 | 0 |
| DR8w2 nM | 1581 | 1140 | 223 | 3769 | ; i |
| DR5w1 1 nM | 741 | 645 | 308 | ; | : |
| DR6w1 9 nM | 522 | 7000 | ; | 569 | 269 |
| DR2w2 β2 nM | 20 | 18 | 299 | : | : |
| DR2w2 β1 nM | 147 | 53 | 3033 | 1597 | : |
| DR3 nM | ŧ | ŧ | ŧ | 167 | 448 |
| DR7 nM | 49 | 34 | 446 | 9259 | ; |
| DR4w4 nM | 281 | 763 | 409 | >8182 | >8182 |
| DR1 nM | 4.2 | 3 | 46 | ; | , |
| Source | MAGE2.102 | MAGE3.102 | DR sup MAGE3.142 | MAGE3.164 | DR3 MAGE3.235 |
| Motif | DR sup | DR sup | DR sup | DR3 | DR3 |
| SEQ ID NO: | 2432 | 2433 | 2434 | 2435 | 2436 |
| Sequence | 39.0283 ESEFQAAISRKMVEL 2432 DR sup MAGE2. | 39.0296 ESEFQAALSRKVAEL | 39.0297 NWQYFFPVIFSKASS 2434 | IELMEVDPIGHLYIF | 39.0407 EDSILGDPKKLLTQH 2436 |
| Peptide | 39.0283 | 39.0296 | 39.0297 | 39.0402 | 39.0407 |

-- indicates binding affinity =10,000nM.